

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 10:08:02 ; Search time 33.0612 Seconds

(without alignments)
1717.821 Million cell updates/sec

Title: US-09-905-666A-75

Perfect score: 939
Sequence: 1 ERNPVVMTHGIGGASFNPG.....NSQVNLSIKEGLNGGILNTN 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315513202 residues

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_rabbit:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	746	79.4	181	2	Q9K5F4	Q9K5F4 bacillus li
2	733	78.1	215	2	Q8VU78	Q8VU78 bacillus sp
3	714	76.0	210	16	P94444	P94444 bacillus sp
4	702	74.3	210	16	P94V55	P94V55 bacillus sp
5	431	45.9	201	2	Q82VDO	Q82VDO paenibacill
6	202	21.5	228	16	Q826T6	Q826T6 streptomyce
7	193	20.6	237	16	Q9RSP6	Q9RSP6 deinococcus
8	180.5	19.2	331	16	Q9KY65	Q9KY65 streptomyce
9	172.5	18.4	286	16	Q82HP7	Q82HP7 streptomyce
10	170	18.1	290	16	Q9S295	Q9S295 streptomyce
11	168	17.9	403	16	Q8RC83	Q8RC83 thermoaer
12	156.5	16.7	202	16	P73372	P73372 synechocyst
13	156	16.6	324	16	Q8NU60	Q8NU60 corynebacte
14	150.5	16.0	339	2	Q96444	Q96444 propionibac
15	149	15.9	352	16	Q8EUC7	Q8EUC7 corynebacte

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1	PRELIMINARY	PRIMER	PRIMER
Q9K5F4	Q9K5F4	181 AA.	181 AA.
AC:Q9K5F4	AC:Q9K5F4		
ID:Q9K5F4	ID:Q9K5F4		
DT:01-OCT-2000 (TREMBLrel. 15, Created)	DT:01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT:01-OCT-2003 (TREMBLrel. 15, Last annotation update)	DT:01-OCT-2003 (TREMBLrel. 15, Last annotation update)		
DE:Lipase (EC 3.1.1.3) (Fragment).	DE:Lipase (EC 3.1.1.3) (Fragment).		
OS:Bacillus licheniformis.	OS:Bacillus licheniformis.		
OC:Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	OC:Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX:NCBI_TaxID=1402;	OX:NCBI_TaxID=1402;		
RN:[1]	RN:[1]		
RP:SEQUENCE FROM N.A.	RP:SEQUENCE FROM N.A.		
RX:PubMed:11339956;	RX:PubMed:11339956;		
RA:Ntangang M.B., Patterson H.G., Van Tonder A., Vergeer W.P.,	RA:Littauer D.,		
RA:Littauer D.,	RA:Littauer D.,		
RT:"Over expression and properties of a purified recombinant Bacillus licheniformis lipase: A comparative report on Bacillus lipases."	RT:"Over expression and properties of a purified recombinant Bacillus licheniformis lipase: A comparative report on Bacillus lipases."		
RL:Enzyme Microb. Technol. 28:705-712(2001).	RL:Enzyme Microb. Technol. 28:705-712(2001).		
DR:EMBL; AJ297356; CAB5850.1;	DR:EMBL; AJ297356; CAB5850.1;		
DR:GO; GO:0016787; F:Hydrolase activity; IEA.	DR:GO; GO:0016787; F:Hydrolase activity; IEA.		
DR:GO; GO:0004806; F:Triacylglycerol lipase activity; IEA.	DR:GO; GO:0004806; F:Triacylglycerol lipase activity; IEA.		
DR:InterPro; IPR002918; Lipase_2.	DR:InterPro; IPR002918; Lipase_2.		
DR:InterPro; IPR000379; Ser est_1.	DR:InterPro; IPR000379; Ser est_1.		
KW:Hydrolase.	KW:Hydrolase.		
PT:NON_TER.	PT:NON_TER.		
SQ:SEQUENCE	SEQUENCE	181 AA.	181 AA.
DR:042AD28D3B0BBB8 CRC64;	DR:042AD28D3B0BBB8 CRC64;		
DR:Best Local Similarity 79.4%; Score 746; DB 2;	DR:Best Local Similarity 79.4%; Score 746; DB 2;		
DR:Length 181;	DR:Length 181;		
DR:Matches 141;	DR:Matches 141;		
DR:Conservative 78.3%; Pred No. 2.8e-51;	DR:Conservative 78.3%; Pred No. 2.8e-51;		
DR:Mismatches 22;	DR:Mismatches 22;		
DR:Indels 0;	DR:Indels 0;		
DR:Gaps 0;	DR:Gaps 0;		

SEQUENCE FROM N.A.

RX:PubMed:11339956;

RA:Littauer D.,

RA:Littauer D.,

RT:"Over expression and properties of a purified recombinant Bacillus licheniformis lipase: A comparative report on Bacillus lipases."

RL:Enzyme Microb. Technol. 28:705-712(2001).

DR:EMBL; AJ297356; CAB5850.1;

DR:GO; GO:0016787; F:Hydrolase activity; IEA.

DR:GO; GO:0004806; F:Triacylglycerol lipase activity; IEA.

DR:InterPro; IPR002918; Lipase_2.

DR:InterPro; IPR000379; Ser est_1.

KW:Hydrolase.

PT:NON_TER.

SQ:SEQUENCE

DR:042AD28D3B0BBB8 CRC64;

DR:Best Local Similarity 79.4%; Score 746; DB 2;

DR:Length 181;

DR:Matches 141;

DR:Conservative 78.3%; Pred No. 2.8e-51;

DR:Mismatches 22;

DR:Indels 0;

DR:Gaps 0;

QY:1 EHNPNVNVGIGGASFNAGIKSYLIVSGQNSRGKLYAVDFWDKTSVNYNGPVLSRFVKK 60

QY:2 ERVr83 thermoanaer

QY:3 P73372 synechocyst

QY:4 Q8NPUVNVGIGGASFNAGIKSYLIVSGQNSRGKLYAVDFWDKTSVNYNGPVLSRFVKK 61

DD:Q96444 propionibac

QY:5 Q8EUC7 corynebacte

QY:6 61 VLDGETGAKKVDIVAHSMGANTLYVKGNGKVNVLGGTNRSTSLSKALPGTDPNQ 120

Db	62	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	121	SEQUENCE FROM N.A. SPECIES=B. subtilis; STRAIN=AC327;
				RX MEDLINE=90128783; PubMed=8973323;
Qy	121	KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGGLNTN	180	RA Yamamoto H., Uchiyama S., Sekiguchi J.; RT "The <i>Bacillus</i> subtilis chromosome region near 78 degrees contains the RT genes encoding a new two-component system, three ABC transporters and RT a lipase." Gene 181:147-151 (1996).
				RT Gene 181:147-151 (1996).
Db	122	KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN	181	RT [3]
				RN SEQUENCE FROM N.A. SPECIES=B. subtilis; STRAIN=168;
Qy	122	KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN	181	RC MEDLINE=9044033; PubMed=9314377;
				RC Kunst F., Ogata N., Moser J., Albertini A.M., Alloni G., Azereedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borrias R., Bourrier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.T., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerison P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Fouger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Haeich J., Harwood C.R., Henaut A., Hilbert H., Hollsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasaiwa Y., Klein C., Kobayashi Y., Koetteler P., Koningstein G., Krogh S., Kumano M., Kurita K., Lapidous A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda A., Mauel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Ouegga B., Park S.H., Parro V., Pohl T.M., Portetelle D., Prescott A.M., Presecan E., Pujo P., Purcell B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha P., Roche B., Rose M., Sadaie Y., Sato T., Scanlan B., Schleich S., Schroeter R., Scoffone P., Shin B.S., Soldo B., Sekiguchi J., Sekovska A., Serror S.J., Serror P., Shiu B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenberg M., Vannier P., Vassarotti A., Viani A., Wambutt R., Wedler B., Wedler H., Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K., Yosumoto K., Yoda K., Yoshida K., Yoshihikawa H., Zumstain B., Yoshikawa H., Datchin A., RT "The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> ." RT Nature 390:249-256 (1997).
Qy	123	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	120	RN [4]
				RN SEQUENCE FROM N.A. SPECIES=B. subtilis; STRAIN=168;
Db	215	SEQUENCE 215 AA; Lipase 2; esterases.	155	RC Kunst F., Ogata N., Yoshihikawa H., Datchin A.; RL Submitted (Nov-1997) to the EMBL/GenBank/DBJ databases.
				DR EMBL: AU430985; CAD4006.1; -. DR EMBL: D78508; BAA1406.1; -. DR EMBL: Z99108; CAB12664.1; -. DR PIR: C6965; C6952. DR GO; GO:0016298; F:lipase activity; IBA. DR GO; GO:00004759; F:serine esterase activity; IBA. DR GO; GO:0016042; F:lipid catabolism; IBA. DR InterPro; IPR000918; Lipase 2. DR InterPro; IPR000379; Ser estErs. DR Pfam; PF01674; Lipase 2;1. DR Hydro-ase; Signal; Complete proteome. KW SIGNAL 1 28 FT CHAIN 29 210 EXTRACELLULAR ESTERASE. SQ SEQUENCE 210 AA; 22363 MW; 4358843F882CC90A CRC64;
Qy	124	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 1 EHNPPVMMHGGASFNAGIKSTLVSQNSRGRKLYADFWDKTGNTNNGPVLSPREVKK 60 Db 36 EHNPPVMMHGGASFNAGIKSTLVSQNSRGRKLYADFWDKTGNTNNGPVLSPREVKK 95 Qy 61 VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ 120 Db 96 VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ 155
Qy	125	KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGGLNTN	180	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 121 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215 Db 156 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	126	KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215	181	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 122 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	127	KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215	181	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 123 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	124	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 125 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGGLNTN 180 Db 156 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	125	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 126 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	126	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 127 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	127	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 128 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	128	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 129 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	129	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 130 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	130	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 131 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	131	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 132 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	132	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 133 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	133	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 134 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	134	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 135 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	135	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 136 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	136	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 137 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	137	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 138 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	138	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 139 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	139	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 140 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	140	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 141 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	141	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 142 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	142	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 143 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	143	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 144 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	144	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 145 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	145	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 146 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	146	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 147 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	147	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 148 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	148	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 149 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	149	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 150 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	150	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Qy 151 KILYTSIYSSADMIVNLYSLKDGAKNVQTHGYGHILLMSQNSLKEGGNGGQNTN 215
Qy	151	VLDKGAKKVDIVAHSMGGANTYYIKNLDGGKIKENVPIGGNGVSSLRGPQDNPQ	155	Query Match 78.1%; Score 733; DB 2; Length 215; Best Local Similarity 77.2%; Pred. No. 3.8e-50; Matches 139; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
				Q

RESULT 6						
Q826T6	PRELIMINARY;	PRT;	228 AA.			
ID Q826T6						
AC						
DT 01-JUN-2003	(TREMBLrel.	24	Created)			
DT 01-JUN-2003	(TREMBLrel.	24	Last sequence update)			
DT 01-OCT-2003	(TREMBLrel.	25	Last annotation update)			
DE Putative lipase.						
GN SAV7089.						
OS Streptomyces avermitilis.						
OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;						
OC Streptomyctaceae; Streptomyces.						
OX NCBI_TAXID=33903;						
RN						
RP SEQUENCE FROM N.A.						
RC STRAIN=MA-4560 / ATCC 31267 / NCIMB 12804 / NRRL 8165;						
RX MEDLINE=21477403; PubMed=11572946;						
RA Omura S., Ikeda H., Ishikawa J., Hananoto A., Takahashi C., Shinozaki M., Nakazawa H., Nakao T., Kikuchi H., Hattori M.;						
RA "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites.",						
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).						
RC SEQUENCE=MA-4560 / ATCC 31267 / NCIMB 12804 / NRRL 8165;						
RX MEDLINE=22603306; PubMed=12652562;						
RA Ikeda H., Ishikawa J., Hananoto A., Shinozaki M., Kikuchi H., Shiba T., Sakai Y., Hattori M., Omura S.;						
RA "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.",						
RL Nat. Biotechnol. 21:525-531 (2003).						
DR EMBL; AP005049; BAC74800.1; -						
DR GO; GO:0003824; F: catalytic activity; IEA.						
DR GO; GO:0016289; F: lipase activity; IEA.						
DR GO; GO:0016012; P: lipid catabolism; IEA.						
DR InterPro; IPR002918; Lipase 2.						
DR InterPro; IPR000379; Ser_esterE.						
DR Pfam; PF01674; Lipase_2.						

01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Putative Secreted Lipase.

GN SCD4799 OR SCD63A.10C.

OC Streptomyces coelicolor.

OC Bacteria; Actinobacter; Actinobacteridae; Streptomyces.

OC Streptomyces; Streptomyctaceae; Streptomyces.

OC NCBI_TaxID=1902;

OX RN

SEQUENCE FROM N.A.

RP STRAIN=A3 (2);

RC Brown S.P., Harris D.;

RA Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

SEQUENCE FROM N.A.

RP STRAIN=A3 (2);

RC Cerdeno A.M., Partill J., Barrell B.G.; Rajandream M.A.;

RA Cerdeno A.M., Partill J., Barrell B.G.; Rajandream M.A.;

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

SEQUENCE FROM N.A.

RP STRAIN=A3 (2);

RC MEDLINE=97003351; PubMed=8843346;

RA Redenbach M., Kieser H.M., Denpaite D., Eichner A., Cullum J.,

RA Kinashi H., Hopwood D.A.;

RA "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3 (2) chromosome.";

RT Mol. Microbiol. 21:77-96 (1996).

RN [4]

SEQUENCE FROM N.A.

RP STRAIN=A3 (2);

RC MEDLINE=2199610; PubMed=12000953;

RA Bentley S.D., Chater K.F., Cerdeno-D.E., Quail M.A., Kieser H.,

RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huaing C.-H., Kieser T., Jarke L., Murphy L., Oliver K., O'Neill S.,

RA Rabbowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

RA Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,

RA Warren T., Witzorre A., Woodward J., Barrell J., Parkhill J.,

RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)." ;

RL Nature 417:141-147 (2002).

DR EMBL: AL939121; CAB92662; 1;

DR GO; GO:0003824; Fatty acid biosynthetic process; activity; IFA.

DR GO; GO:0016298; Fatty acid biosynthesis; activity; IFA.

DR GO; GO:0016042; Fatty acid catabolism; IFA.

DR InterPro; IPR002918; Lipase 2.

DR InterPro; IPR008262; Lipase_AS.

DR InterPro; IPR000379; Ser estri.

DR Pfam; PRO0674; Lipase 2; 1.

DR PROSITE; PS00120; LPASE_SER; 1.

KW Complete proteome.

SQ SEQUENCE 331 AA; 35137 MW; 3E0E77A687747211 CRC64;

Query 4 PVMVHGIGGSFENFAIGKSYLVSQWSRGKLYAVDFWDKTGTNYANGPVLSRFVKKVLD 63

Best Local Similarity 19.4%; Score 180.5%; DB 16; Length 331;

Matches 54; Conservative 41; Mismatches 29; Gaps 6;

DR 115 PVVLLGFIDNSFVLLRRLQHQ-RHAEISNYSPLCDIRTAELLGRHIEICE 172

DR 116 DPGKILYTSIYSSADMMVNLSK--LD---GAKVQIHRVGHTG 157

DR 173 RFGSERDVVGHSLLGGLIARYVQRGGDLRVRTVLTGPFHTGKVVPLANAHPVROM 232

Qy 4 PVMVHGIGGSFENFAIGKSYLVSQWSRGKLYAVDFWDKTGTNYANGPVLSRFVKKVLD 63

Best Local Similarity 26.7%; Score 218.0%; DB 16; Length 331;

Matches 54; Conservative 41; Mismatches 29; Gaps 6;

DR 115 PVVLLGFIDNSFVLLRRLQHQ-RHAEISNYSPLCDIRTAELLGRHIEICE 172

DR 116 DPGKILYTSIYSSADMMVNLSK--LD---GAKVQIHRVGHTG 157

DR 173 RFGSERDVVGHSLLGGLIARYVQRGGDLRVRTVLTGPFHTGKVVPLANAHPVROM 232

Qy 114 -PGT-----DPGKILYTSIYSSADMMVNLSK--LD---GAKVQIHRVGHTG 157

DR 233 RPSAVTEELTPAPGGRTRFVFSWSDLDR-VMDPLETACUDHPDLSVQNRVSGIGHLA 291

Qy 158 LLMSQNSLNSLILKEGLNGGLT 179

DR 292 LPYHPATGALDPTAGET 313

RESULT 1.0

Q82HP7 PRELIMINARY; PRT; 286 AA.

ID Q82HP7

AC Q82HP7- (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DB Putative Lipase.

GN SAV2461.

OS Streptomyces avermitilis.

OC Bacteria; Actinobacteria; Actinomycetidae; Streptomyces.

OC Streptomyctaceae; Streptomyces.

OX NCBI_TaxID=339303;

RN [1]

SEQUENCE FROM N.A.

RP ATCC 31267 / NCIMB 12804 / NRRL 8165;

RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

RC SEQUENCE FROM N.A.

RP STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

RC MEDLINE=21477403; PubMed=11592948;

RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,

RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osoneo T.,

RA Kikuchi H., Shiba T., Sakai Y., Hattori M.;

RT "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites.";

RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).

RL [2]

RN SEQUENCE FROM N.A.

RP STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

RC MEDLINE=22608306; PubMed=126592562;

RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,

RA Sakai Y., Hattori M., Omura S.;

RT "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitillii.";

RL Nat. Biotechnol. 21:526-531 (2003).

DR EMBL: AP005035; BAC1173.1;

DR GO: GO:003824; Fatty acid biosynthetic activity; IFA.

DR InterPro; IPR008262; Lipase_AS.

DR InterPro; IPR000379; Ser estri.

DR PROSITE; PS00120; LPASE_SER; 1.

KW Complete proteome.

SQ SEQUENCE 286 AA; 30720 MW; 1C5C9B2F12B2DD9 CRC64;

Query 4 PVMVHGIGGSFENFAIGKSYLVSQWSRGKLYAVDFWDKTGTNYANGPVLSRFVKKVLD 63

Best Local Similarity 18.4%; Score 172.5%; DB 16; Length 286;

Matches 51; Conservative 41; Mismatches 75; Indels 35; Gaps 5;

DR 76 PVVLLGFIDNSFVLLRRLQHQ-RQKESLNYSPLCDIRTAELLGRHIEICE 133

Qy 64 ETGAKKVDIVAHSMGGANTLYTIKNDGGKVENVVTLLGGTNRSTSALK----- 113

DR 134 RTGHARYDVGHSLLGGLIARYVQCLGGDIRVRLTGLTPHSGRPVALANAHPIVROM 193

Query 4 PVMVHGIGGSFENFAIGKSYLVSQWSRGKLYAVDFWDKTGTNYANGPVLSRFVKKVLD 63

Best Local Similarity 25.2%; Pred. No. 1e-05;

Matches 51; Conservative 41; Mismatches 75; Indels 35; Gaps 5;

DR 76 PVVLLGFIDNSFVLLRRLQHQ-RQKESLNYSPLCDIRTAELLGRHIEICE 133

Qy 64 ETGAKKVDIVAHSMGGANTLYTIKNDGGKVENVVTLLGGTNRSTSALK----- 113

DR 134 RTGHARYDVGHSLLGGLIARYVQCLGGDIRVRLTGLTPHSGRPVALANAHPIVROM 193

Query 4 PVMVHGIGGSFENFAIGKSYLVSQWSRGKLYAVDFWDKTGTNYANGPVLSRFVKKVLD 63

Best Local Similarity 26.7%; Pred. No. 2.9e-06;

Matches 54; Conservative 41; Mismatches 78; Indels 29; Gaps 6;

DR 115 PVVLLGFIDNSFVLLRRLQHQ-RHAEISNYSPLCDIRTAELLGRHIEICE 172

DR 116 DPGKILYTSIYSSADMMVNLSK--LD---GAKVQIHRVGHTG 157

DR 173 RFGSERDVVGHSLLGGLIARYVQRGGDLRVRTVLTGPFHTGKVVPLANAHPVROM 232

Qy 114 -PGT-----DPGKILYTSIYSSADMMVNLSK--LD---GAKVQIHRVGHTG 157

DR 233 RPSAVTEELTPAPGGRTRFVFSWSDLDR-VMDPLETACUDHPDLSVQNRVSGIGHLA 291

Qy 158 LLMSQNSLNSLILKEGLNGGLT 179

DR 292 LPYHPATGALDPTAGET 313

RESULT 1.1

Q93295 PRELIMINARY; PRT; 290 AA.

ID Q93295

AC Q93295; (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Putative secreted Lipase.

GN SCO1735 OR SCL11-24C.

OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
 OC Streptomyces; Streptomyctinae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1] —
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Saunders D.; Harris D.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN SEQUENCE FROM N.A.
 RP Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=9000551; PubMed=8843436;
 RA Redenbach M.; Kieser H.M.; Denapaitre D.; Eichner A.; Cullum J.;
 RA Kinashi H.; Hopwood D.A.;
 RT "A set of ordered cosmid and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=21996410; PubMed=120000953;
 RA Bentley S.D.; Chater K.F.; Cerdano-Tarraga A.-M.; Challis G.L.;
 RA Thomson N.R.; James K.D.; Harris D.E.; Kieser H.;
 RA Harper D.; Bateman A.; Brown S.; Chandra G.; Chen C.W.; Collins M.;
 RA Cronin A.; Fraser A.; Goble A.; Hidalgo J.; Hornsby T.; Howard S.;
 RA Huang C.; Kieser T.; Larke L.; Murphy L.; Oliver K.; O'Neil S.;
 RA Rabinowitzsch E.; Rajandream M.A.; Rutledge K.; Rutter S.;
 RA Seeger K.; Saunders D.; Sharp S.; Squares R.; Taylor K.;
 RA Warren T.; Wetzorrek A.; Woodward J.; Barrell B.G.; Parkhill J.;
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL99110; CAB50950.1; -.
 DR PIR; T36757; T36757.
 DR HSSP; Q054819; 1TAH.
 DR GO; GO:0003824; F: catalytic activity; IEA.
 DR GO; GO:0016042; F:lipase activity; IEA.
 DR InterPro; IPR002918; Lipase 2.
 DR InterPro; IPR00379; Ser ester.
 DR Pfam; PF01674; Lipase_2_1.
 KW Complete proteome.
 SQ SEQUENCE 290 AA; 30496 MW; D568508350F7432 CRC64;
 Query Match 18.1%; Score 170; DB 16; Length 290;
 Best Local Similarity 29.2%; Pred. No. 17e-05; Indels 50; Gaps 8;
 Matches 56; Conservative 28; Mismatches 58;
 QY 4 PYVMVHGIGGASF-NPAGIKSYLVSGWSRGLKLYAVDFWDKGTGTYNNGPV-----L 54
 DB 56 PIVLVHGTFGNSVDNWGLAPLKLKGNGYC--VFSLDYQQLGPVKEKSABO! 112
 QY 55 SRFVKKVLDETGAKKYDIVAHSMGGANTLYKVN-----L 54
 DB 113 AAHVDKVLAATGATEDGLVGSQGGMNPYTLKFLGGAEVNALVGIASNHGTLGSLT 172
 QY 111 XALP-----GTDPNQKILYTSIYSSADMIVMNYL 139
 DB 173 RLLPYFPGAEDLNEHTPALAQVWSSDVLRLNAGGDTVEGVRTVLTAKYDEVVTPYR 232
 QY 140 SK-LD--GAKNV 148
 DB 233 GQFLDGPVSYRV 244

RESULT 13
 P33372 PRELIMINARY; PRT; 202 AA.
 AC P73372 PRELIMINARY; PRT; 202 AA.
 DT 01-FEB-1997 (TRIMBrel. 02, Created)
 DT 01-FEB-1997 (TRIMBrel. 02, Last sequence update)
 DT 01-OCT-2003 (TRIMBrel. 25, Last annotation update)
 DE Hypothetical protein (PMGA).
 GN SLL1969.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 RN NCBI_TaxID=1148;
 RP SEQUENCE FROM N.A.
 DR EMBL; AL99110; CAB50950.1; -.
 RA Kaneko T.; Sato S.; Kotani H.; Tanaka A.; Asamizu E.; Nakamura Y.;
 RA Miyajima N.; Hirayama M.; Sugiyama N.; Sasaki S.; Kimura T.;
 RA Hosouchi T.; Matsuno A.; Muraki A.; Nakazaki N.; Natuo K.; Okumura S.;
 RA Shimpou S.; Takeuchi C.; Wada T.; Watanabe A.; Yamada M.; Yasuda M.;
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PC6803. II. Sequence determination of the
 entire genome and assignment of potential protein-coding regions";
 RT DNA Res. 3:109-136(1996).
 RN SEQUENCE OF 27-202 FROM N.A.
 RA Ihara Y.; Ikeuchi M.;

RL SUBMITTED (JUN-1991) TO EMBL/Genbank/DBDJ databases.
DR EMBL: D90905; BAA17403.1; -.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 10:01:57 ; Search time 9.18367 seconds
 (without alignments)
 1020.575 Million cell updates/sec

Title: US-09-905-666A-75

Perfect score: 93.9

Sequence: 1 EHNPVVMVHGIGGASFNFAG.....NSQVNNSLKEGLNGGILNTN 180

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	884	94.1	212	1	LIP_BACSU	P37957	bacillus su
2	129	12.8	358	1	LIP_PSEGL	Q05489	pseudomonas
3	118.5	12.6	364	1	LIP_BURCE	P22088	burkholderi
4	118.5	12.6	364	1	LIP_PSESS	P25275	pseudomonas
5	103	12.1	312	1	LIP_VIBCH	P15493	vibrio chol
6	96.5	10.3	737	1	LIP_ENTFA	P37710	enterococcus
7	96.5	10.3	681	1	LIP_STAAM	Q99qxD	staphylococ
8	94.5	10.2	688	1	LIP_STAEP	Q2510	staphylococ
9	94.5	10.1	293	1	MHPC_ECOLI	P7044	escherichia
10	90	9.6	662	1	MHEI_SCHNA	P46508	schistosoma
11	89.5	9.5	690	1	LIP_STAAW	P10335	staphylococ
12	89.5	9.5	690	1	LIP_STAAW	Q8nyC	staphylococ
13	88	9.4	431	1	ENO_SHEON	Q8erb0	shewanella
14	86	9.2	277	1	BPHD_PSESI	P17548	pseudomonas
15	86	9.2	1052	1	RT32_ACTPL	P55131	actinobacil
16	85.5	9.1	605	1	AOR_PYRUF	P51739	pyrococcus
17	85	9.1	326	1	TGL2 YEAST	P54857	saccharomy
18	84.5	9.0	351	1	ADH_GLOBE	P25984	lactocidium
19	84	8.9	268	1	BSL2_MYCP	P25311	mycoplasma
20	83.5	8.9	373	1	ACOC_ALCEU	P27747	alcaligenes
21	83.5	8.9	1113	1	MGA2 YEAST	P40578	saccharomy
22	82.5	8.8	234	1	PUR7_STRA3	Q8etX2	streptococc
23	81.5	8.7	277	1	LIP_BSEFR	P08658	pseudomonas
24	81	8.6	1754	1	MPME_CHLTR	Q84418	chlamydia
25	80.5	8.6	415	1	YEGM_ECOLI	P76397	escherichia
26	80.5	8.6	607	1	AOR_PFRAB	Q9v035	pyrococcus
27	80	8.5	313	1	YK74 YEAST	P28321	saccharomy
28	79.5	8.5	236	1	PUR7_LACI	Q68830	lactococcus
29	79.5	8.5	245	1	FLGF_CAUCL	P06171	caulobacter
30	79.5	8.5	286	1	P47229	burkholderi	
31	79.5	8.5	288	1	Y134_BURCE	Q50599	mycobacteri
32	79.5	8.5	306	1	MIAA_BORBU	P51761	borrelia
33	79.5	8.5	331	1	KRAK_DROME	Q18391	drosophila

ALIGNMENTS

RESULT 1
 LIP_BACSU STANDARD; PRT; 212 AA.
 ID LIP_BACSU STANDARD; PRT; 212 AA.
 AC P37957; O34644; 01-OCT-1994 (Rel. 30, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
 GN LIPA OR LIP OR BSU2700.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=1423;
 RN [1]

SEQUENCE FROM N.A.
 STRAIN=168;

RC MEDLINE=92329538; PubMed=9274031;
 RA Dartois V., Baulard A., Schanck C., Colson C.;
 RT "Cloning, nucleotide sequence and expression in Escherichia coli of a lipase gene from Bacillus subtilis 168";
 RL Biochim. Biophys. Acta 1131:253-260(1992);
 RN [2]
 SEQUENCE FROM N.A.
 RC MEDLINE=98044033; PubMed=3384377;
 RA Azavedo V., Bertiro M.G., Bessieres P., Boloian A., Albertini A.M., Alloni G., Kuntz F., Ogasawara N., Moser I., Bessieres P., Boloian A., Borchert S., Borelli S.C., Bron S., Brionell S., Bourrier L., Braun M., Brignell S.C., Brion S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Conneron I.P., Cummings N.J., Daniel R.A., Denizot F., Devre K.M., Dusterhoff A., Ehrlich S.D., Bimmermann P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Fouger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleton N., Ghim S.Y., Glaser P., Goffeau A., Golightly J., Grandi G., Guiseppi G., Guy B.J., Hage K., Haleck J., Harwood C.R., Honaut A., Hilbert H., Holzapfel S., Hosono S., Hulio M.F., Itaya M., Jones L., Joris B., Kararamata D., Katahara Y., Klaarr-Bleichard M., Klein C., Kobayashi Y., Koettner P., Konigstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Puigc B., Purnelle B., Rapport G., Rey M., Reynolds S., Rieger M., Rivoira C., Rocha E., Rose B., Sadaie Y., Sato T., Scanlan E., Schilich S., Schroeter R., Scoffone F., Setiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,

FT MUTAGEN 324 324 H->A: COMPLETE LOSS OF ACTIVITY
 FT CONFLICT 40 40 A -> W (IN REF. 2).

FT TURN 43 44

FT STRAND 50 53

FT TURN 61 62

FT HELIX 65 67

FT TURN 70 71

FT HELIX 72 78

FT TURN 79 80

FT STRAND 83 86

FT TURN 89 90

FT STRAND 97 98

FT HELIX 100 115

FT TURN 116 116

FT STRAND 120 125

FT TURN 126 126

FT HELIX 127 138

FT HELIX 140 142

FT STRAND 143 149

FT TURN 153 154

FT HELIX 157 168

FT TURN 170 171

FT TURN 173 174

FT HELIX 176 188

FT TURN 191 193

FT HELIX 196 204

FT TURN 205 206

FT HELIX 208 217

FT TURN 221 222

FT STRAND 223 223

FT TURN 226 228

FT STRAND 231 231

FT STRAND 235 238

FT TURN 239 240

FT STRAND 241 248

FT STRAND 250 250

FT STRAND 253 259

FT TURN 260 261

FT STRAND 262 267

FT TURN 275 275

FT HELIX 276 279

FT HELIX 281 294

FT TURN 295 297

FT STRAND 301 301

FT STRAND 306 306

FT HELIX 307 310

FT STRAND 314 315

FT STRAND 320 320

FT TURN 324 325

FT HELIX 326 328

FT TURN 329 333

FT TURN 337 338

FT HELIX 342 356

FT TURN 357 358

FT SEQUENCE 358 AA, 36928 MW, FE7B5D7A22EC6B4B CRC64;

Query Match 13.8%; Score 129.5%; DB 1; Length 358;

Best Local Similarity 34.8%; Bred. No. 0.00081;

Matches 40; Conservative 16; Mismatches 42; Indels 17; Gaps 6;

SQ SEQUENCE

4 PYVMVHGIGGASENFA-----GKSYLVSQGWSRGKLYAVD---FWDKGTGNNANGV 53
 49 PVTLVHGLAGTD-KFANVWDNYGIGQSDLQSHG---AKVYVANLGSQFDGPN-GRGQ 103

54 LSRFVKVLDETGAKYDIDVAHSMGGANTLYIKHLDGGHRYENVVTLGTRNTRST 108

55 LLAYVKVQVLAATGATQNLIGHSGQGLTSRYA--AVAPQLVAVSFTTGPFRGS 156

56

RESULT 3
 ID LIP BURCE
 ID - LIP BURCE
 AC P22088;

DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lipase precursor (BC 3.1.1.3) (Triacylglycerol lipase).
 GN LIPA.
 OS Burkholderia cepacia (Pseudomonas cepacia).
 OC Bacteria; Proteobacteria; Burkholderiales;
 Burkholderiaceae; Burkholderia.
 NCBI TaxID=292;
 OX [1]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 45-66.
 RP STRAIN=DSM 3959;
 RC STRAIN=DSM 3959;
 RX MEDLINE=91100343; PubMed=1987151;
 RA Jørgensen S., Skov K.W., Diderichsen B.;
 RT "Cloning, sequence, and expression of a triacylglycerol lipase from Pseudomonas cepacia: lipase production in heterologous hosts requires two Pseudomonas genes";
 RT J. Bacteriol. 173:559-567(1991).
 RL [2]
 RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=97184684; PubMed=9032074;
 RA Kim K.K., Song H.K., Shin D.H., Hwang K.Y., Suh S.W.;
 RT "The crystal structure of a triacylglycerol lipase from Pseudomonas cepacia reveals a highly open conformation in the absence of a bound inhibitor.";
 RT Structure 5:173-185(1997).
 RL [3]
 RN X-RAY CRYSTALLOGRAPHY.
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=97184685; PubMed=9032074;
 RA Schrag J.D., Li Y., Cygler M., Lang D., Burgdorf T., Hecht H.-J., Schrag J.D., Rydel T.J., Oliver J.D., Strickland L.C., Schmid P., Schomburg D., Rydel P., Dunaway C.M., Larson S.B., Day J., McPherson A.;
 RT "The open conformation of a Pseudomonas lipase.";
 RL Structure 5:187-202(1997).
 CC -I CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a fatty acid anion.
 CC -I COFACTOR: Requires calcium.
 CC -I SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS LIPASE FAMILY.

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 CC
 CC DR EMBL; M58494; AAA50466.1; -.
 CC DR PDB; 1Q1I; 15-MAY-97.
 CC DR PDB; 2I1P; 12-MAR-97.
 CC DR PDB; 3I1P; 16-JUN-97.
 CC DR PDB; 1RQD; 22-AUG-01.
 CC DR PDB; 4I1P; 19-AUG-98.
 CC DR InterPro; IPR000073; A/b hydrolase.
 CC DR InterPro; IPR008462; Lipase.
 CC DR InterPro; IPR000379; Ser estrs.
 CC DR Pfam; PF00561; abhydrolase_1.
 CC DR PROSITE; PS00120; LIPASE_SRP; 1.
 CC KW Hydrolase; Lipid degradation; signal; calcium; 3D-structure.
 CC FT SIGNAL 1 44
 CC FT CHAIN 45 364
 CC FT ACT SITE 131 131
 CC FT ACT SITE 286 286
 CC FT ACT SITE 330 330
 CC FT TURN 48 49
 CC FT STRAND 55 58
 CC FT TURN 61 62
 CC FT STRAND 66 67
 CC FT TURN 68 70
 CC FT STRAND 71 72
 CC FT TURN 75 76
 CC FT HELIX 77 83

RX	MEDLINE=92118228; PubMed=1368739;
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HELIX	105
105	120
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HELIX	145
145	147
STRAND	148
148	154
TURN	TURN
158	159
HELIX	162
162	171
TURN	TURN
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TURN	TURN
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HELIX	178
178	194
TURN	TURN
196	197
HELIX	204
204	210
TURN	TURN
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HELIX	213
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TURN	TURN
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313	316
STRAND	STRAND
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HELIX	332
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HELIX	348
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86	RESULT 5
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87	54 PIIIVHGLSGTID-KYAGLEY---WYQIODELQONGATVYANLSQFQSDDCAN-GRG 106
87	52 PVLSRFVKVLDETGAKVDTIYAHNSGANTLYYIKNLDGKNYENVVLTGGNRT 108
87	52 EQLAYVTKVLAATGATKVNLYGHSGQGLTSRYVA-AVAPDLVASVTTGPHRG 161
87	107 EQLAYVTKVLAATGATKVNLYGHSGQGLTSRYVA-AVAPDLVASVTTGPHRG 161
88	89
89	Query Match
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89	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
89	RESULT 4
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90	52 PVLSRFVKVLDETGAKVDTIYAHNSGANTLYYIKNLDGKNYENVVLTGGNRT 108
90	52 EQLAYVTKVLAATGATKVNLYGHSGQGLTSRYVA-AVAPDLVASVTTGPHRG 161
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92	Query Match
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92	29.3%; Score 118.5; DB 1; Length 364;
92	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
92	RESULT 5
92	LIP_VIBCH
92	STANDARD:
92	PRT: 312 AA.
93	4 PVMVHGIGGASFNAGIKSYLVSQW-----SRGKLYAVD--FWDKTGTNTNG 51
93	54 PIIIVHGLSGTID-KYAGLEY---WYQIODELQONGATVYANLSQFQSDDCAN-GRG 106
93	52 PVLSRFVKVLDETGAKVDTIYAHNSGANTLYYIKNLDGKNYENVVLTGGNRT 108
93	52 EQLAYVTKVLAATGATKVNLYGHSGQGLTSRYVA-AVAPDLVASVTTGPHRG 161
93	107 EQLAYVTKVLAATGATKVNLYGHSGQGLTSRYVA-AVAPDLVASVTTGPHRG 161
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95	Query Match
95	Best Local Similarity
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95	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
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95	STANDARD:
95	PRT: 312 AA.
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98	Query Match
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98	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
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98	LIP_VIBCH
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98	PRT: 312 AA.
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99	54 PIIIVHGLSGTID-KYAGLEY---WYQIODELQONGATVYANLSQFQSDDCAN-GRG 106
99	52 PVLSRFVKVLDETGAKVDTIYAHNSGANTLYYIKNLDGKNYENVVLTGGNRT 108
99	52 EQLAYVTKVLAATGATKVNLYGHSGQGLTSRYVA-AVAPDLVASVTTGPHRG 161
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101	Query Match
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101	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
101	RESULT 5
101	LIP_VIBCH
101	STANDARD:
101	PRT: 312 AA.
102	4 PVMVHGIGGASFNAGIKSYLVSQW-----SRGKLYAVD--FWDKTGTNTNG 51
102	54 PIIIVHGLSGTID-KYAGLEY---WYQIODELQONGATVYANLSQFQSDDCAN-GRG 106
102	52 PVLSRFVKVLDETGAKVDTIYAHNSGANTLYYIKNLDGKNYENVVLTGGNRT 108
102	52 EQLAYVTKVLAATGATKVNLYGHSGQGLTSRYVA-AVAPDLVASVTTGPHRG 161
102	107 EQLAYVTKVLAATGATKVNLYGHSGQGLTSRYVA-AVAPDLVASVTTGPHRG 161
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104	Query Match
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104	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
104	RESULT 5
104	LIP_VIBCH
104	STANDARD:
104	PRT: 312 AA.
105	4 PVMVHGIGGASFNAGIKSYLVSQW-----SRGKLYAVD--FWDKTGTNTNG 51
105	54 PIIIVHGLSGTID-KYAGLEY---WYQIODELQONGATVYANLSQFQSDDCAN-GRG 106
105	52 PVLSRFVKVLDETGAKVDTIYAHNSGANTLYYIKNLDGKNYENVVLTGGNRT 108
105	52 EQLAYVTKVLAATGATKVNLYGHSGQGLTSRYVA-AVAPDLVASVTTGPHRG 161
105	107 EQLAYVTKVLAATGATKVNLYGHSGQGLTSRYVA-AVAPDLVASVTTGPHRG 161
106	107
107	Query Match
107	Best Local Similarity
107	29.3%; Score 118.5; DB 1; Length 364;
107	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
107	RESULT 5
107	LIP_VIBCH
107	STANDARD:
107	PRT: 312 AA.
108	109
109	Query Match
109	Best Local Similarity
109	29.3%; Score 118.5; DB 1; Length 364;
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109	LIP_VIBCH
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109	PRT: 312 AA.
110	111
111	Query Match
111	Best Local Similarity
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111	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
111	RESULT 5
111	LIP_VIBCH
111	STANDARD:
111	PRT: 312 AA.
112	113
113	Query Match
113	Best Local Similarity
113	29.3%; Score 118.5; DB 1; Length 364;
113	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
113	RESULT 5
113	LIP_VIBCH
113	STANDARD:
113	PRT: 312 AA.
114	115
115	Query Match
115	Best Local Similarity
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115	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
115	RESULT 5
115	LIP_VIBCH
115	STANDARD:
115	PRT: 312 AA.
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117	Query Match
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117	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
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117	LIP_VIBCH
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117	PRT: 312 AA.
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119	Query Match
119	Best Local Similarity
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119	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
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121	STANDARD:
121	PRT: 312 AA.
122	123
123	Query Match
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123	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
123	RESULT 5
123	LIP_VIBCH
123	STANDARD:
123	PRT: 312 AA.
124	125
125	Query Match
125	Best Local Similarity
125	29.3%; Score 118.5; DB 1; Length 364;
125	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
125	RESULT 5
125	LIP_VIBCH
125	STANDARD:
125	PRT: 312 AA.
126	127
127	Query Match
127	Best Local Similarity
127	29.3%; Score 118.5; DB 1; Length 364;
127	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
127	RESULT 5
127	LIP_VIBCH
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127	PRT: 312 AA.
128	129
129	Query Match
129	Best Local Similarity
129	29.3%; Score 118.5; DB 1; Length 364;
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129	LIP_VIBCH
129	STANDARD:
129	PRT: 312 AA.
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133	PRT: 312 AA.
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135	RESULT 5
135	LIP_VIBCH
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135	PRT: 312 AA.
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137	Query Match
137	Best Local Similarity
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137	LIP_VIBCH
137	STANDARD:
137	PRT: 312 AA.
138	139
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139	Best Local Similarity
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139	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
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141	PRT: 312 AA.
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145	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
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145	PRT: 312 AA.
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147	LIP_VIBCH
147	STANDARD:
147	PRT: 312 AA.
148	149
149	Query Match
149	Best Local Similarity
149	29.3%; Score 118.5; DB 1; Length 364;
149	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
149	RESULT 5
149	LIP_VIBCH
149	STANDARD:
149	PRT: 312 AA.
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151	RESULT 5
151	LIP_VIBCH
151	STANDARD:
151	PRT: 312 AA.
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153	Query Match
153	Best Local Similarity
153	29.3%; Score 118.5; DB 1; Length 364;
153	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
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153	LIP_VIBCH
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153	PRT: 312 AA.
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155	PRT: 312 AA.
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157	Best Local Similarity
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161	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
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163	LIP_VIBCH
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165	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
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167	Matches 35; Conservative 19; N:smatches 42; Indels 21; Gaps 6;
167	RESULT 5
167	LIP_VIBCH
167	STANDARD:
167	PRT: 312 AA.
168	169
169	

Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

[3] SEQUENCE FROM N.A. STRAIN-EL TOR N16961 / Serotype O1; MEDLINE=20106833; PubMed=105301; Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umamaheswaram L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.; Birmolaeva M.D., Vamathevan J., Bais S., Qin H., Dragoi I., Sellers P.; McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.; "DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*." Nature 406:477-483 (2000).

RL NATURE 406:477-483 (2000).
 CC -!- FUNCTION: CATALYZES THE SYNTHESIS OF MACROCYCLIC LACTONES IN ANHYDROUS ORGANIC SOLVENTS.
 CC -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a fatty acid anion.
 CC -!- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase Family.

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 CC EMBL; Y00577; CAA68339.1; -.
 DR AE00362; AAF96133.1; ALT_INIT.
 DR PIR; S15911; S15911.
 DR HSSP; P22058; 3LIP.
 DR TIGR; VCA0221; -.
 DR InterPro; IPR000073; A/b-hydrolase.
 DR InterPro; IPR000379; Ser esterase.
 DR Pfam; PF00561; abhdrolase_1.
 DR PROSITE; PS00120; LIPIASE_SER_1.
 DR Hydrolase; Lipid degradation; Potential, SIGNAL¹ 22; LACTONIZING_LIPASE_CHAIN²³ 312; LACTONIZING_LIPASE.
 FT ACT_SITE¹¹⁰ 110; CHARGE_RELAY_SYSTEM (BY SIMILARITY).
 FT ACT_SITE²³⁸ 238; CHARGE_RELAY_SYSTEM (BY SIMILARITY).
 FT ACT_SITE²⁷⁸ 278; CHARGE_RELAY_SYSTEM (BY SIMILARITY).
 KW SEQUENCE^{312 AA;} 32995 MW; 96AA000A07A568CD CRC64;

FT Best_Local_Similarity^{29.6%}; Score¹¹⁴; DB¹; Length³¹²; Matches³⁷; Conservative²⁷; Mismatches⁴⁹; Indels¹²; Gaps⁷;

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 Db 37 KKVLDGEGAKKDYIAHSMGANTTYYTKLDGENKVENVYVLTGGRTR-STATSKALPGTD 117
 Qy 59 SELLAVTIGKRNVLIGHSHGP-TIRYVASV-RPDLVAVSITGGVHKGSAVADLVRGVI 150
 Qy 118 PNQKI 122
 Db 151 PGSV 155

RESULT 6
 ID ALYS_ENTFA
 AC P37701
 DT 01-OCT-1994 (Rel. 3.0, Created)
 DT 10-OCT-2003 (Rel. 4.2, Last sequence update)
 DT 10-OCT-2003 (Rel. 4.2, Last annotation update)
 DE Autolysin Precursor (EC 3.2.1.-) (Peptidoglycan hydrolase)

DE (Beta-glycosidase).
 RN DE0799.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBITaxID=1351;
 RN [1] -
 RP SEQUENCE FROM N.A.
 RX MEDLINE=135349; PubMed=1579432;
 RA Bellevau C., Potvin C., Tridel J., Asselin A., Bellemare G.; "Cloning, sequencing, and expression in *Escherichia coli* of a *Streptococcus faecalis* autolysin."
 RT J. Bacteriol. 173:15619-15622 (1991).
 RL R1
 RN [2] -
 RP SEQUENCE FROM N.A.
 RC STRAIN ATCC 700802 / ATCC 700802;
 RX MEDLINE=22550857; PubMed=12663927;
 RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R., Read T.D., Routs D.E., Eisen J.A., Gill S.R., Heidelberg J.F., Tettelin H., Dodson R.J., Umamaheswaram L., Brinkac L., Beanan M., Daugherty S., Debey R.T., Durkin S., Kolonay J., Madupu R., Nelson W., Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H., Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.; "Role of mobile DNA in the evolution of vancomycin-resistant *Enterococcus faecalis*." Science 299:2071-2074 (2003).
 CC -!- FUNCTION: Hydrolyzes the cell wall of *E.faecalis* and M. lyoedeticus. May play an important role in cell wall growth and cell separation.
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- DOMAIN: LysM repeats are thought to be involved in peptidoglycan binding.
 CC -!- SIMILARITY: Belongs to family 73 of glycosyl hydrolases.
 CC -!- SIMILARITY: Contains 6 LysM repeats.

CC -----
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 CC -----
 DR EMBL; M85002; AA67325.1; -.
 DR EMBL; A601699; AA008613.1; -.
 DR PIR; A38109; A38109.
 DR TIGR; EBF0799; -.
 DR InterPro; IPR002901; Amidase_4.
 DR InterPro; IPR002482; LysM_4.
 DR Pfam; PF01832; Amidase_4; 1.
 DR Pfam; PF01476; LysM_5.
 DR SMART; SM00257; LysM_6.
 DR SM00044; LZ22; 1.
 KW Hydrolase; Glycosidase; Bacteriolytic enzyme; Cell wall; Cell division; Septation; Repeat; Signal; Complete proteome.
 FT SIGNAL¹ 53
 FT CHAIN⁵⁴ 737
 FT REPEAT⁵⁵ 85
 FT REPEAT⁵⁶ 405
 FT REPEAT⁵⁷ 431
 FT REPEAT⁵⁸ 473
 FT REPEAT⁵⁹ 499
 FT REPEAT⁶⁰ 541
 FT REPEAT⁶¹ 567
 FT REPEAT⁶² 609
 FT REPEAT⁶³ 633
 FT REPEAT⁶⁴ 675
 FT REPEAT⁶⁵ 737
 FT CONFLICT⁶⁶ 85
 FT CONFLICT⁶⁷ 118
 FT CONFLICT⁶⁸ 143
 FT CONFLICT⁶⁹ 417
 FT CONFLICT⁷⁰ 449
 FT CONFLICT⁷¹ 476
 FT CONFLICT⁷² 484
 FT CONFLICT⁷³ 567
 SQ 737 AA; 77025 MW; ABB1BD50AC7507 CRC64;
 SEQUENCE 737 AA; 77025 MW; ABB1BD50AC7507 CRC64;

Query Match

11.0%; Score 103; DB 1; Length 737;

Best Local Similarity 23.3%; Pred. No. 0.34;
Matches 48; Conservative 32; Mismatches 90; Indels 36; Gaps 7;

Qy 10 GIGGASFNFGAIKS-YLVSGQNSRCKL--YAYDENDKTGTYNNNGPVL---SRFVKK- 60
Db 416 GIGGASFNFGAIKS-YLVSGQNSRCKL--YAYDENDKTGTYNNNGPVL---SRFVKK- 60

Qy 61 VLDETGAKKDIVAHSMCGANTLYYKNDGGNKV----- 95
Db 476 ASGNTGGSNNGGNNNQSGNTTYTISGDTLUNKIAAQYGSVANLRSWNGISGDLIFAG 535

Qy 96 ENVYLGGINTRSTSKALPGTDPNQKLYTSYSSADMIVNVLKSLDGMNVQTHGVGH 155
Db 536 QKIIYKGTGSNTGCGSSNGSNNNQSGNT-TYTIKSGDTLUNKISAAQFQGSVANLQAWN 594

Qy 156 I-GLIMNSOVSNTSLIKEINGGGINTN 180
Db 595 IGSGLIFAGOKIIVKGANGSNTN 620

RESULT 7
LIP_STAAM STANDARD PRT; 681 AA.
ID LIP_STAAM PRT; 681 AA.
AC Q99X0; PRT; 681 AA.
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DB Lipase precursor (EC 3.1.1.3). (Glycerol ester hydrolase).
GN LIP OR GHE OR SAV271 OR SA2463.
OS Staphylococcus aureus (strain Mu50) / ATCC 700699, and
Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
OC NCBI_TaxID=158878, [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699, and N315;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Ouchi A., Aoki K.-O., Nagai Y., Ito T., Lian J.-O., Hosoya A.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kubara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Ohshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of meticillin-resistant Staphylococcus
aureus." Lancet 357:1225-1240 (2001).
RL 3671225-1240(2001).
CC -!- FATTY ACID ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC -!- SUBCELLULAR LOCATION: Secreted (BY similarity).
CC -!- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC family.

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CC DR EMBL; AP0346; BAB5833.1; -
CC DR EMBL; AP00338; BAB43769.1; -
CC DR PIR; G30075; G90075; -
CC DR InterPro; IPR00587; Gpos_YIRK.
CC DR InterPro; IPR00B262; Lipase_AS.
CC DR InterPro; IPR000379; Ser esters.
CC DR TIGRFAM; YIRK01168; YIRK Signal; 1.
CC DR PROSITE; PS00120; LIPASE SER; 1.
CC DR PROSITE; PS00120; LIPASE SER; 1.
CC KW Hydrolase; Lipid degradation; Zymogen; Signal; Complete proteome.
FT SIGNAL 1 35 POTENTIAL.
PROPEP 36 291 BY SIMILARITY.

DR	InterPro; IPR005877; Gpos_YSIRK.
DR	InterPro; IPR008222; Lipase AS.
DR	InterPro; IPR000379; Ser esters.
Pfam;	PF04650; YSIRK_Bigal_1.
DR	TIGRFAMS; TIGR01168; YSIRK signal; 1.
DR	PROSITE; PS00120; LIPASE SER; 1.
KW	Hydrolease; Lipid degradation; Zmogen; Signal; Complete proteome.
SIGNAL	1 35 POTENTIAL.
PROPEL	1 35 REMOVED IN THE MATURE FORM.
PROPEL	36 302 LIPASE.
CHAIN	303 688 CHARGE RELAY SYSTEM (BY SIMILARITY).
ACT_SITE	418 648 CHARGE RELAY SYSTEM (BY SIMILARITY).
ACT_SITE	648 96 W -> L (IN REF. 1).
CONFLICT	120 120 W -> G (IN REF. 1).
CONFLICT	120 96 W -> G (IN REF. 1).
SEQUENCE	688 AA; 77343 MW; 6C95DB3A78AR86F6 CRC64;
Query Match	10.2%; Score 95.5; DB 1; Length 688;
Best Local Similarity	22.7%; Pred. No. 1.4;
Matches	47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;
Qy	3 NPVVMHGIGGASPNFAGIKSYLVSQGWSRGKLYAVDFDKTGNNYANGPVLSRFVKVVL 62
Ddb	327 NPVSILTHYNGDKNN--I-FQDLEENGYEASISAF---GSNYDRAVELYYIKGGR 379
Qy	63 DETGA-----KKVDIVAHSSGGANTLYIKNL----- 89
Ddb	380 VDYGAAHAAKYGHERRYKTYEGVYKDWKPQKIHVLGHNSMG-QTIRQLEFLRHLGNPPE 438
Qy	90 -----DGG -NKVENVNVTLGGTRNRTTSKALPGTDPNQKLYTSSAD 132
Ddb	439 VEYQHQHGGESPLYQGHNNMVSSSTTLTPHNGTHASDILG--NEAVRQLND-- 492
Qy	133 MIVVNYLSQLDGAKVQI-HGVGHIGL 158
Ddb	493 -----VGKMYGNKDSSRVDFGLEFWCL 513
RESULT	9
MHPC_ECOLI	STANDARD; PRT; 293 AA.
MHPC_ECOLI	AC P77044; P71204; P77205;
AC	01-NOV-1997 (Rel. 35, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	2-hydroxy-6-ketona-2,4-dienedioic acid hydrolase (EC 3.7.1.-).
MHPC	GN OR B0149.
OS	Escherichia coli.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Escherichia.
OX	NCBI_TaxID=562;
RN	[1] _TAXID=562;
RN	SEQUENCE FROM N.A.
RP	STRAN=N-K12 / C5520;
RC	Ferrandez A.; Garcia J.L.; Diaz E.;
RA	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RL	[3]
RN	SEQUENCE FROM N.A.
RP	STRAN=N-K12 / MG1655;
RC	MEDLINE=91426617; PubMed=9278503;
RA	Blattner F.R.; Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA	Riley M., Collado-Vides J., Glasner J.D., Rose C.K., Mayhew G.F.,
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA	Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12.";
RT	Science 27:1453-1474 (1997).
RL	[4]
RN	SEQUENCE FROM N.A.
RP	STRAN=N-K12 / MG1655.

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CC -!- MISCELLANEOUS: The expression of *Staphylococcus* lipase is negatively regulated by bacteriophage lysogenization (lipase conversion). Belongs to the AB hydrolase superfamily. Lipase family.

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CC EMBL: M12715; AA26633.1; -

CC PIR: A24545; A24545.

CC HSSP: P00192; 256B.

CC InterPro; IPR00577; Gpos_VSIRK.

CC InterPro; IPR00862; Lipase_AS.

CC InterPro; IPR00079; Ser_enders.

CC Ptm; P04655; VSIRK_Signal; 1.

CC TIGRFAM; TIGR01168; VSIRK signal; 1.

CC PROSITE; PS0120; LIPASE_SER; 1.

CC KW Hydrolase; Lipid degradation; Zymogen; Signal.

CC SIGNAL; 1

CC FT PROPEP; 38 295 LIPASE.

CC FT CHAIN; 296 690 HYDROPHOBIC.

CC FT DOMAIN; 311 690 CHARGE RELAY SYSTEM (BY SIMILARITY).

CC FT ACT SITE; 412 412 CHARGE RELAY SYSTEM (BY SIMILARITY).

CC FT ACT SITE; 645 645 CHARGE RELAY SYSTEM (BY SIMILARITY).

CC SQ SEQUENCE; 690 AA; 763.88 MW; B8E33654D0E01A3B CRC64;

CC Query Match; 9.5%; Score 90; DB 1; Length 690; Best Local Similarity 23.3%; Prod. No. 4.5%; Gaps 8; Matches 47; Conservative

CC QY 4 PVMYHGI-----GGASFNFGAKSYLVSQGWSRGKLYAYFDWKTCGTN 4.7

CC Db 306 PYVEFHGFLGLVGDNAAPALYPNTWGGNPKF---VIEELRKQGTVHQSVAH----GGSN 358

CC QY 4.8 YNNGPVLSRVEKVKYLDDEGTA-----KCDIVAHSMGGANT 82

CC Db 359 YDRAVELYYIGGRVDGAHAAYKGHERYGTQYKTMENWPGKCKVHLVGHSMGGGTI 418

CC QY 83 LYVIRNLDGKVE-----NVTIILGGNR---SITSKALP-----GTD 117

CC Db 419 RLMFPLRNGKKEIAYHKAQGGEISPLFTGGHNNMVSITTLATPHNGSQAADKFGNTE 478

CC QY 1.18 PNQKLYT-----SIYSSADM 133

CC Db 479 AVRKMFALNRFMGKNSNDL 500

CC RESULT 12

CC LIP_STAAW STANDARD PRT; 690 AA.

CC ID LIP_STAAW STDAW STANDARD PRT; 690 AA.

CC AC QBNICP; AC

CC DT 15-MAR-2004 (Rel. 43, Created)

CC DT 15-MAR-2004 (Rel. 43, Last sequence update)

CC DT 15-MAR-2004 (Rel. 43, Last annotation update)

CC DT 15-MAR-2004 (Rel. 43, Last annotation update)

CC DE Lipase precursor (EC 3.1.1.3) (Glycerol ester hydrolase).

CC GN LIP OR GEH OR MW0297.

CC OS *Staphylococcus aureus* (strain MW2).

CC OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.

CC NCBI_TaxID:196620;

CC RN SEQUENCE FROM N.A.

CC RP MEDLINE=8119581; PubMed=300394;

CC RX Lee C.Y.; Iandolo J.J.;

CC RT "Lysogenic conversion of *staphylococcal* lipase is caused by insertion of the bacteriophage L51a genome into the lipase structural gene.";

CC RT J. Bacteriol. 166:85-91(1986).

CC RN PROCESSING, AND SEQUENCE OF 296-307.

CC RP STRAIN=TEN 5;

CC MEDLINE=92193269; PubMed=15482322;

CC RA Rollif J.; Normark S./

CC RA "In vivo processing of *Staphylococcus aureus* lipase.";

CC RT J. Bacteriol. 174:1844-1847(1992).

CC CC "- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a fatty acid anion.

CC CC "- SUBCELLULAR LOCATION: Secreted.

RL Lancet 359:1819-1827(2002).
 CC -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
 CC fatty acid anion.
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
 CC family.
 CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -!- EMBL; AP04923; BAA94162.1;
 DR InterPro; IPR005877; Gpos_YSRK.
 DR InterPro; IPR008262; Lipase_MS.
 DR InterPro; IPR000379; Ser_esters.
 DR Pfam; PF04650; YSRK_signal; 1.
 DR TIGRFAMS; TIGR0116; YSRK signal; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 DR Hydrolase; Lipid degradation; Zymogen; Signal; Complete proteome.
 KW SIGNAL 1 37 POTENTIAL.
 FT PROPEP 38 295 BY SIMILARITY.
 FT CHAIN 296 690 LIPASE (BY SIMILARITY).
 FT ACT SITE 412 412 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT SITE 645 645 CHARGE RELAY SYSTEM (BY SIMILARITY).
 SQ SEQUENCE 690 AA; 76522 MW; 36FFB5EDBB434CCA CRC44;
 Qy 4 PVMVHGI-----GGASPNFAGIKSYLVSGNSRGHLAYVDFWDXKTGTN 47
 Qy Best Local Similarity 9.5%; Score 89.5%; DB 1; Length 690;
 Matches 47; Conservative 21; Mismatches 55; Indels 79; Gaps 8;
 Db 306 PIVFVHGLVGDNAPALPNYNGNKKR--VIEELRKQGIVNQASVSAF-- GSN 358
 Qy 48 YNGGPVLSRFVKKVLDGTGA-----KVDIVAHSMGGANT 82
 Qy 359 YDRAVELYYTIGGRVYDGAHAAXKYGHERYKGTYKIMPNWBPGKRVHLVHSMGQT 418
 Qy 83 LYIYKNDGKKEV-----NVTMIGGTNR--STATSCLP----- GTD 117
 Db 419 RLMEFFLRNGKEETAYKRAHGGELSPPLFTGGHNMVASITTLATPHNGSQADKFGNT 478
 Qy 118 PNOKILY-----SIYSSADM 133
 Qy 479 AVRKMFLANLRFMGKYSNLD 500
 Db -!- ENO_SHBON STANDARD; PRT; 431 AA.
 ENO_SHEON STANDARD; PRT; 431 AA.
 AC QBE BRO;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
 DE Glycerate hydro-lyase).
 GN ENO OR SO340
 OS Shewanella oneidensis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Alteromonadaceae; Shewanella.
 OX NCBI_TAXID=70863;
 RP RESULT 13
 STRAIN-MR-1;
 RC PubMed=22367686; PubMed=12368813;
 RX Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
 RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
 RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolenjai J.F.,
 RA

RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Lee C.,
 RA Vanithavan J., Weidman J., Gill J., Utterback T.R., McDonald L.A.,
 RA Mueller J., Khouri H., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.,
 RA "Genome sequence of the dissimilatory metal ion-reducing bacterium
 RT Shewanella oneidensis".
 RT Nat. Biotechnol. 20:1118-1123 (2002).
 CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
 CC H(2)O.
 CC -!- COFACTOR: Magnesium is required for catalysis and for stabilizing
 CC the dimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the enolase family.
 CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC use by non-profit institutions as long as its content is in no
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 CC or send an email to license@isb-sib.ch).
 CC -!- EMBL; A2015780; AN56437.1; ALT_INIT.
 DR TIGR; SG3440; -
 DR InterPro; IPR000941; -
 DR Pfam; PF00113; enolase; 1.
 DR PROSITE; PS00164; ENOLASE; 1.
 DR ACT SITE 159 159 Complete proteome.
 DR PRINTS; PR0395; enolase; N; 1.
 DR PROBEM; PD000902; Enolase; 1.
 DR TIGRFAMS; TIGR01160; eno; 1.
 DR PROSITE; PS00164; ENOLASE; 1.
 DR KW Lyase; Glycolysis; Magnesium; Complete proteome.
 FT METAL 246 246 BY SIMILARITY.
 FT METAL 289 289 MAGNESIUM (BY SIMILARITY).
 FT METAL 316 316 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 431 AA; 45686 MW; 3D7FLA065832B312 CRC64;
 Qy 3 NPVYV-MYHIGGASFNPAFAGIKSYLVSGNSRGHLAYVDFWDXKTGTN 49
 Qy 18 NPVYEAHFALEGG---PIGMAA--AEQASTGSREALERDGDSRYLGKVLTAVANV 71
 Qy 50 NGPYVSLRFSVKKVLDGTGA-----KVDIVAHSMGGANT 124
 Qy 72 NGPRTALIGK--DATAEELQIMIDGTEN-- KDKEGANAI-LAVSLAAKAKAA 124
 Qy 110 SKALP-----GTD-----PNQKILYTSIYSSADMVYNLISKDQSKDLSRGLGKVLTAVANV 153
 Qy 125 FKGMPFLYHIAEINGTPQYAMFVPMNLLGEHADNVDIQLQEFMVQPVGAKNFR---- 180
 Qy 154 GHIGLMMQSVNSLVIKEGLNGGGLNTN 180
 Qy 181 --EALRMDGABEFLTKLQHKGKLS 205
 Qy RESULT 14
 BPHD PS051 STANDARD; ERT; 277 AA.
 ID BPHD PS051
 AC P1758;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydro-lase (EC 3.7.1.-).
 OS Pseudomonas sp. (strain K5102).
 OC Bacteria; Proteobacteria.
 OX NCBI_TAXID=111.

OX NCBI_TaxID=307;

RN [1] SEQUENCE FROM N.A.

RP MEDLINE=89213965; PubMed=2540155;

RX Jansen R., Briaire J., Kamp E.M., Gielkens A.L.J., Smits M.A.;

RA Kimbara K., Hashimoto T., Fukuda M., Koana T., Takagi M., Oishi M., Yano K.; "Cloning and sequencing of two tandem genes involved in degradation of 2,3-dihydroxybiphenyl to benzoic acid in the polychlorinated biphenyl-degrading soil bacterium *Pseudomonas* sp. strain KKS102.";

RT J. Bacteriol. 171:2740-2747(1989).

RL JAPAN. Degradation of biphenyls and polychlorobiphenyls (PCB) to benzoic acid and chlorobenzoic acids.

CC - SIMILARITY: STRONG, TO E.COLI M9PC.

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CC DR EMBL: M26433; AAA25751.1; -.

CC DR PIR: B32312; ESPSSK; A/b hydrolase.

CC DR InterPro: IPR00073; AB_hydrolase.

CC DR InterPro: IPR0003089; AB_hydrolase.

CC DR InterPro: IPR000379; Ser esterases.

CC DR PFAM: PF00561; abhydrolase_1.

CC DR PRINTS: PR00111; ABHYDROLASE.

CC DR Aromatic hydrocarbons catabolism; Hydrolase.

KW BY SIMILARITY

FT ACT SITE 112 112

SQ SEQUENCE 277 AA; 30253 MW; B0C74618681AD1E CRC64;

Query Match Score 86; DB 1; Length 277;

Best Local Similarity 27.1%; Pred. No. 3;

Matches 21; Conservative 21; Mismatches 44; Indels 48; Gaps 9;

QY 5 VAVYHIGGGSFENPAGIKSYLVSGWSR----GKL----YAVDEFWDKTGTYNN-----50

Db 36 VIMLHG-GGGG----AG-----GWSNTYRNIGPFPVAGIYRVLIDPAGFENKSDTVMD 83

QY 51 --GPGVLSRVRKVLDETAKKVDIVAHNSGGANTLYIKKNDGGKVNVENTVTLGCTNRS 107

Db 84 EQRLGVNARSGVKGMNDVLGIEKAHLGVNGGAGALNPA---LEYPBRTGKLLIMG----136

QY 108 TTSKALPGTDPNQKLYTTSYSSADMIVNNYLSKL 142

Db 137 -----PGG-----LGNSUFTANVMEGKILPKL 159

RESULT 15

DT 01-OCT-1996 (Rel. 34, Created)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE RTX-III toxin determinant A from serotype 8 (APX-IIIa) (Cytolysin IIIA) (CLY-IIIa).

DE OS *Actinobacillus pleuropneumoniae* (Haemophilus pleuropneumoniae).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Actinobacillus.

OX NCBI_TaxID=715;

RN SEQUENCE FROM N.A.

RC STRAIN=405 / Serotype 8;

RC MEDLINE=95012630; PubMed=79227703;

RX Jansen R., Briaire J., van Geel A.B.M., Kamp E.M., Gielkens A.L.J., Smits M.A.;

RA "Generic map of the *Actinobacillus pleuropneumoniae* RTX-toxin (Apx) operons: characterization of the ApxIII operons.";

RL Infect. Immun. 62:4411-4418(1994).

[2] SEQUENCE FROM N.A.

RP SPAIN=Serotype 8;

RC MBLINE=93162836; PubMed=8432615;

RX Jansen R., Briaire J., Kamp E.M., Gielkens A.L.J., Smits M.A.;

RA "Cloning and characterization of the *Actinobacillus pleuropneumoniae* RTX-toxin III (ApxIII) gene.";

RT Infect. Immun. 61:947-954(1993).

CC -!- FUNCTION: Does not have hemolytic activity but shows a strong cytotoxicity towards alveolar macrophages and neutrophils.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- CC DOMAIN: The Gly-rich region is probably involved in binding or cytolytic calcium, which is required for target cell-binding or cytolytic activity (By similarity).

CC -!- CC DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (By similarity).

CC -!- CC DOMAIN: Palmitylated by apxIIIIC. The toxin only becomes active when modified (By similarity).

CC -!- CC SIMILARITY: Belongs to the RTX Prokaryotic toxin family.

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CC DR EMBL: X80055; CAA6358.1; -.

CC DR EMBL: X68815; CAA68711.1; -.

CC DR PIR: B49219; B49219.

CC DR InterPro: IPR001343; Hemolysin_Ca_bind.

CC DR InterPro: IPR003995; RxXA.

CC DR Pfam: PF00553; HemolysinCabinD; 6.

CC DR PRINTS: PR00313; CABNDNGRPT.

CC DR PRINTS: PR01488; RTXTOXINA.

CC DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 3.

CC DR Toxin: Cytolysin; Hemolysin; Receptor; Calcium; Transmembrane; Lipoprotein;

CC DR Palmitate; Palmitate.

CC DR FT TRANSEM 248 265 POTENTIAL.

CC DR FT TRANSEM 275 334 POTENTIAL.

CC DR FT TRANSEM 372 418 POTENTIAL.

CC DR DOMAIN 754 859 7 X REPEATS, GLY-RICH.

CC DR REPEAT 754 759 1.

CC DR REPEAT 763 768 2.

CC DR REPEAT 772 777 3.

CC DR REPEAT 781 786 4.

CC DR REPEAT 790 795 5.

CC DR REPEAT 799 804 6.

CC DR REPEAT 808 813 7.

CC DR REPEAT 827 832 8.

CC DR REPEAT 836 841 9.

CC DR REPEAT 845 850 10.

CC DR REPEAT 854 859 11.

CC SQ SEQUENCE 1052 AA; 112809 MW; F83A8F25A8FD8758 CRC64;

Query Match Score 86; DB 1; Length 1052;

Best Local Similarity 22.1%; Pred. No. 15;

Matches 33; Conservative 23; Mismatches 47; Indels 46; Gaps 7;

QY 41 WDRGTGTYNNNPVLSRFRVRYLDEGAKKTDIVAHSMGGANTLYIKNLDGGKVNVT 100

Db 922 WKEGNKYNHK-----IEQIVDVKNGRK-----ITAENLG-----TYFXNAPKADNLNYAT 967

QY 101 LGGTNRSTTSKALPGTDPNQKLYTTSYSSADMIVNNYLSKL 158

Db 968 KEDQDNNSNL-----SLKTELSKIN-----AGNFGWAKQNTGINT 1005

QY 159 -LMNSQSONSLIKEG-----LNGGGIAT 179

Db 1006 AALNNENKIISSANTFATSQGGSGMGT 1034

Search completed: April 23, 2004, 10:12:31
Job time : 10.1837 secs

8. A; Reference number: S74322; MUID: 97061201; PMID: 8905231
 A; Accession: S77556
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Residues: 1-202 <KAN>
 A; Cross-references: EMBL:D0905; GB:AB001339; NID:91653360; PIDN:BA417403.1; PID:d101813
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C; Genetics:
 A; Start codon: GTG

Query Match 16.7% Score 156.5; DB 2; Length 202;
 Best Local Similarity 32.7% Pred. No. 9e-06; Indels 7; Gaps 3;
 Matches 36; Conservative 24; Mismatches 43; Gaps 3;

Qy 1 EHNPPVWVIGGASFNPAIGKSYLVSQGWSRGKLYAVDFWDKTKTNYNNGPVLSRFVVK 60
 Db 7 DRHPVVLVIGIYDTRAKTATMDFLTGKWS--VHCLDLYPNQDS--TSLALLAEQVQ 61

Qy 61 VLDEBTGA--KKYDIVAHSMGGANTLYYKINLDGGKVNENTVTLGGTNRST 108
 Db 62 YIDDRPAPPQPVDLIGFSNGLVTRYLQRUGGERVRRITISAPNQGT 111

RESULT 6
 AE1175 hypothetical protein alr1352 [imported] - Nostoc sp. (strain PCC 7120)
 C; Species: Nostoc sp. PCC 7120
 A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C; Date: 14-Dec-2001 #sequence_change 14-Dec-2001 #text_change 09-Dec-2002
 C; Accession: AE1175
 R; Kaneko, T.; Nakanura, Y.; Wolk, C.P.; Kuritz, T.; Saamoto, S.; Watanabe, A.; Iriuchi, N.; Nakazaki, T.; Shimojo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A; Accession: ABB1807; MUID: 21555285; PMID:11759840

RESULT 8
 T24853 hypothetical protein T12A7.4 - Caenorhabditis elegans
 C; Species: Caenorhabditis elegans
 A; Date: 15-Oct-1999 #sequence_change 15-Oct-1999 #text_change 15-Oct-1999
 C; Accession: T24853
 R; Lennard, N.
 submitted to the EMBL Data Library, June 1996
 A; Accession number: 219913
 A; Accession: T24853
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Species: Caenorhabditis elegans
 A; Residues: 1-371 <VIL>
 A; Cross-references: EMBL:Z73911; PIDN:CAA98139.1; GSPDB:GN00022; CBSP:T12A7.4
 C; Genetics:
 A; Gene: CEP124853

Query Match 15.3% Score 144; DB 2; Length 211;
 Best Local Similarity 26.5% Pred. No. 0.0001; Indels 40; Gaps 8;
 Matches 54; Conservative 34; Mismatches 76; Gaps 8;

Qy 1 EHNPPVWVIGGASFNPAIGKSYLVSQGWSRGKLYAVDFWDKTKTNYNNGPVLSRFVVK 59
 Db 7 QRNPVPLVIGIYDTRAKTATMDFLTGKWS--VHCLDLYPNQDS--TSLALLAEQVQ 57

Qy 60 KVLDSS---TGAKKVDIVAHSMGGANTLYYKINLDGGKVNENTVTLGGTNRST---SK 111
 Db 70 QVADYVCACTTPEPFDIYDTPVPMAYTLRQWHTYTLNLP-----NNGEAPLNVLAQ 57

Qy 112 ALPG--TDPN-----QKLYTISYSSAD-MIVMNTLSKLQDGAKNQVQIHWV 153
 Db 118 QHPGCVQMRNNSLEQDNLNDVQMLEQINFTSINTPDLMIPTSSKMPVGKELTIYV 177

Qy 154 GHIGLMN---SOYNSLKEGLN 173
 Db 178 LHSNMLKDFRSIEAVAAALAEPIIN 201

RESULT 7
 T20712 hypothetical protein F10F2.3 - Caenorhabditis elegans
 C; Species: Caenorhabditis elegans
 C; Date: 15-Oct-1999 #sequence_change 15-Oct-1999 #text_change 20-Jun-2000
 C; Accession: T20712
 R; Coles, L.

Query Match 14.3% Score 134.5; DB 2; Length 371;
 Best Local Similarity 25.7% Pred. No. 0.00096; Indels 51; Gaps 8;
 Matches 47; Conservative 21; Mismatches 64; Indels 51; Gaps 6;

Qy 1 EHNPPVWVIGGASF-----NFGAGKSYLVSQGWSRGKLYAVDFWDKTKT-----46
 Db 41 EKEPVIFHSGSDTAFLTQPLATESRSRSTQYELQNTTEAELYATTGDTWGSMSMLDT 100

Qy 47 -----NYANGVVLSRVFKVLDETGAKYDIVAHSMGGANTLYYK-----NLDG-----91
 Db 101 YSTIHQCGNQJYLRLRPLERAVIGYPSKAKRTDIAINSVGVBLMRKTVKGGTLLIGDGNCTIG 160

Qy 92 ---GKRVENVYVTLGGTNR-----TTSKALPQTGPDKPNQKLYTISYSSADMIVMN 137
 Db 161 PPLGAKYDVTFLGIAGENFGCVCVQLAQTYVPAWCNAALDGLYPG-----YTCQDQLMCG 212

Qy 138 YLS 140
 Db 213 YTS 215

RESULT 8
 T24853 hypothetical protein T12A7.4 - Caenorhabditis elegans
 C; Species: Caenorhabditis elegans
 A; Date: 15-Oct-1999 #sequence_change 15-Oct-1999 #text_change 15-Oct-1999
 C; Accession: T24853
 R; Lennard, N.
 submitted to the EMBL Data Library, June 1996
 A; Accession number: 219913
 A; Accession: T24853
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Species: Caenorhabditis elegans
 A; Residues: 1-371 <VIL>
 A; Cross-references: EMBL:Z73911; PIDN:CAA98139.1; GSPDB:GN00022; CBSP:T12A7.4
 C; Genetics:
 A; Gene: CEP124853

Query Match 14.3% Score 134.5; DB 2; Length 371;
 Best Local Similarity 32.3% Pred. No. 0.0013; Indels 35; Gaps 8;
 Matches 43; Conservative 22; Mismatches 35;

Qy 3 NPVVMYHIGGASF---NFA---GKSYLIVSQGWSRGKLYAVDFWDKTKT-----NYN 49
 Db 111 DEVIFRGGNSDAALTANNEFTGWTITVQFLQCYTGLHLYGTS-WGNTNTTAVERHD 169

Qy 50 NGPV--LISRFVVKVLDETGAKKVDIVAHSMGGANTLY-----YIKNLDG-----G 92
 Db 170 CTVTFRLRKFEAVMDTGAQINIIHSNG--VTLLRKVILGGYINADDGSCNIGKBLG 227

Qy 93 NKVENVYVTLGGT 105
 Db 228 NKVRVIGIAGAN 240

T26657 hypothetical protein Y38E10A.9 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans* sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C;Accession: T26657
 R;Wallis, J.
 A;Submitted to the EMBL Data Library, September 1999
 A;Reference number: 220252
 A;Accession: T26657
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Cross-references: EMBL:AL110484; PIDN:CA854398.1; CBSP:Y38E10A.9
 A;Experimental source: clone Y38E10A
 A;Genetics:
 A;Gene: CBSP:Y38E10A.9
 A;Introns: 63/2; 221/2; 261/3
 C;Superfamily: *Caenorhabditis elegans* hypothetical protein C09E8.2

Query Match 14.2%; Score 133; DB 2; Length 286;
 Best Local Similarity 25.4%; Pred. No. 0.0012;
 Matches 49; Conservative 25; Mismatches 65; Indels 54; Gaps 5

Qy 4 PVMVHGIGGASNFAGIKSYLVSGQWSRGKLYAVDFWDKGITGTYNNNGPVLISRFYKVK--
 Db 66 EIVLHGTTNGAGTFPQAAFRANGWSEETVYATTYGDAGVTTATNVKMLCEYVQQIRN
 Qy 62 ---LDETGAKKVDIVAHSMGGANTLYYIKNLDGGKVNENVTLG-----G
 Db 126 MIIAYNAFTQOKVNTGYSMSSPIAR---KAIIGGCAENTVQLGAPLTSIETYISVAG
 Qy 104 TNRST-----TSAKALPG-----TDPNQKILYT---SIYSSAD----
 Db 183 ANRGTSCLCDLIFAPLYVPTCNTKNGLKCSSDFLTDIRSVSSAYEGQYIFSYGPSPDDKVG
 Qy 133 NIVMNTYLSKLQGA 145
 Db 243 NTVCGRVSRIIDGA 255

RESULT 10
 T27932 hypothetical protein ZK617.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T27932
 R;White, S.
 A;Submitted to the EMBL Data Library, May 1996
 A;Reference number: 220442
 A;Accession: T27932
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Cross-references: EMBL:Z733897; PIDN:CAA980652.1; GSPDB:GN00022; CBSP:ZK617
 A;Experimental source: clone ZK617
 A;Genetics:
 A;Gene: CBSP:ZK617.2
 A;Map position: 4
 A;Introns: 62/2; 121/3; 288/2

Query Match 13.9%; Score 130.5; DB 2; Length 344;
 Best Local Similarity 25.9%; Pred. No. 0.0024;
 Matches 52; Conservative 27; Mismatches 71; Indels 51; Gaps 5

Qy 4 PVMVHGIGGASNFAGIKSYLVSGQWSRGKLYAVDFWDKGITGTYNNNGPVLIS-----
 Db 65 PVMVHGIGGASNFAGIKSYLVSGQWSRGKLYAVDFWDKGITGTYNNNGPVLIS-----
 Qy 56 RFRKVKDVEGAKKVDIVAHSMGGANTLYYI---KNDLGGN-----KVNENVTLGG
 Db 124 RFLETVLTQKQDVGYSMOSPIARKKALLOGKCDNPVYALGPISLHSRSHVITYISVAG
 Qy 104 TNPSSTSKALP-----GTPONOKT-----YTSV-----SSADMIVNXYL-----

Db	184	AKQGSQCALPFIDCNMKTELMCNISKFLEDINWFNEYEGSYKAFNLASTADFVV-GTNA	242
Qy	140	----SKLDGAKNVQFHGVGH	155
Db	243	CGTKASSEFTGHEWKVEGRNH	263
RESULT 11			
A;Accession:	A48952	tricetylglycerol lipase (EC 3.1.1.3) precursor - <i>Pseudomonas glumae</i>	
C;Species:	<i>Pseudomonas glumae</i>		
C;Date:	10-Sep-1999	#sequence_revision 10-Sep-1999 #text_change 10-Sep-1999	
C;Accession:	A48532 ; S36248 ; S36291		
R;Frenken, L.G. ; Egmond, M.R. ; Batesburg, A.M. ; Bos, J.W. ; Visser, C. ; Verrips, C. ; Appl. Environ. Microbiol. 58, 3787-3791, 1992			
A;Title:	Cloning of the <i>Pseudomonas glumae</i> lipase gene and determination of the reference number: A48952; MUID:9311910; PMID:1476423		
A;Accession:	A48952		
A;Status:	preliminary		
A;Molecule type:	DNA		
A;Residues:	1-358 <FRB>		
A;Cross-references:	EMBL:X70354 ; NID:g49205 ; PIDN:CAA49812_1 ; PID:g49206		
A;Experimental source:	PG1		
A;Note:	sequence extracted from NCBI backbone (NCIN:121572 ; NCIP:121573)		
R;Frenken, L.G.J. ; Bos, J.W. ; Visser, C. ; Mueller, W. ; Tommassen, J. ; Verrips, C. ; Mol. Microbiol. 9, 579-589, 1993			
A;Title:	An accessory gene, <i>lipB</i> , required for the production of active <i>Pseudomonas</i> triacylglycerol lipase		
A;Reference number:	S36248 ; MUID:94018632 ; PMID:8412704		
A;Accession:	S36248		
A;Molecule type:	DNA		
A;Residues:	316-558 <PR2>		
A;Cross-references:	EMBL:X70354		
C;Genetics:			
A;Gene:	lipA		
C;Superfamily:	<i>Pseudomonas</i> triacylglycerol lipase		
C;Keywords:	carboxylic ester hydrolase; extracellular protein		
Qy	4	PUVVRGGGASINPA-----GKXVLYVSGWSRQKLYAVD--FWDKTKTNNYNGPV	53
Db	49	PVILVHGLAGTD-KFANTVDDWYQGICSDQSGH--AKVYANLSSQFDGPN-GRGEQ	103
Qy	54	LSRFPVQVLDETGAKVVDIVASMGANTLYTKNDQGKVNENVTLGGNTRST	108
Db	104	LLAIVKQVLLAETKVNLLGQGTSRYVA-AYAPQDQVASYTGTGPHRGS	156
RESULT 12			
A;Accession:	A97027	hydrolase of alpha/beta superfamily, probable membrane associated lipase [imported]	
C;Species:	<i>Clostridium acetoacetylicum</i>		
C;Date:	14-Sep-2001	#sequence_revision 14-Sep-2001 #text_change 14-Sep-2001	
C;Accession:	A97027		
R;Nolling, J. ; Breton, G. ; Omelchenko, M.V. ; Markarova, K.S. ; Zeng, Q. ; Gibson, J. ; Daly, M.J. ; Bennett, G.N. ; Koonin, E.V. ; Smith, D.R. ; J. Bacteriol. 183, 4823-4831, 2001			
A;Title:	Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium <i>Clostridium acetoacetylicum</i>		
A;Reference number:	A96900 ; MUID:21359325 ; PMID:21359325		
A;Accession:	A97027		
A;Status:	preliminary		
A;Molecule type:	DNA		
A;Residues:	1-479 <KUR>		
A;Cross-references:	GB:AE001437 ; PIDN:AAK79004_1 ; PID:g1502939 ; GSPDB:GN00168		
A;Experimental source:	<i>Clostridium acetoacetylicum</i> ATCCB824		
A;Gene:	CAK1028		
Query Match	13.4%	Score 126; DB 2;	Length 479;
Best Local Similarity	22.0%	Pred. No. 0.0086;	

Search completed: April 23, 2004, 10:15:21
Job time : 113.398 secs

GenCore version 5.1.6
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OM Protein - protein search, using sw model

Run on: April 23, 2004, 10:14:03 ; Search time 25.3571 Seconds

(without alignments)
1407.510 Million cell updates/sec

Title: US-09-905-666A-75

Sequence: 1 EHNPVYVNHGGASFNFGA.....NSQVNLIKEGLNGGILNTN 180

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpa/US07_PUBCOMB.PEP:*
 2: /cn2_6/ptodata/2/pubpa/PTC_NEW_PUB.PEP:*
 3: /cgn2_6/ptodata/2/pubpa/US06_PUBCOMB.PEP:*
 4: /cgn2_6/ptodata/2/pubpa/US06_PUBCOMB.PEP:*
 5: /cn2_6/ptodata/2/pubpa/PTUS_NEW_PUB.PEP:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93.9	100.0	180	10	US-09-905-666A-75
2	92.7	98.7	180	10	US-09-905-666A-104
3	92.5	98.5	180	10	US-09-905-666A-78
4	92.4	98.4	180	10	US-09-905-666A-98
5	92.3	98.3	180	10	US-09-905-666A-76
6	92.3	98.3	180	10	US-09-905-666A-108
7	92.2	98.2	180	10	US-09-905-666A-87
8	92.0	98.0	180	10	US-09-905-666A-77
9	92.0	98.0	212	10	US-09-905-666A-58
10	92.0	98.0	212	10	US-09-905-666A-59
11	92.0	98.0	212	13	US-10-028-247-4
12	91.9	97.9	180	10	US-09-905-666A-99
13	91.7	97.7	180	10	US-09-905-666A-82
14	91.7	97.7	180	10	US-09-905-666A-107
15	91.4	97.3	180	10	US-09-905-666A-102

Sequence 103, App	10	US-09-905-666A-103
Sequence 105, App	10	US-09-905-666A-105
Sequence 62, App	10	US-09-905-666A-62
Sequence 11, App	10	US-09-905-666A-81
Sequence 100, App	10	US-09-905-666A-100
Sequence 101, App	10	US-09-905-666A-101
Sequence 55, App	10	US-09-905-666A-55
Sequence 61, App	10	US-09-905-666A-61
Sequence 97, App	10	US-09-905-666A-97
Sequence 84, App	10	US-09-905-666A-84
Sequence 86, App	10	US-09-905-666A-86
Sequence 88, App	10	US-09-905-666A-88
Sequence 60, App	10	US-09-905-666A-60
Sequence 94, App	10	US-09-905-666A-94
Sequence 106, App	10	US-09-905-666A-106
Sequence 80, App	10	US-09-905-666A-80
Sequence 84, App	10	US-09-905-666A-84
Sequence 85, App	10	US-09-905-666A-85
Sequence 83, App	10	US-09-905-666A-83
Sequence 96, App	10	US-09-905-666A-96
Sequence 89, App	10	US-09-905-666A-89
Sequence 95, App	10	US-09-905-666A-95
Sequence 90, App	10	US-09-905-666A-90
Sequence 93, App	10	US-09-905-666A-93
Sequence 69, App	10	US-09-905-666A-69
Sequence 63, App	10	US-09-905-666A-63
Sequence 91, App	10	US-09-905-666A-91
Sequence 95, App	10	US-09-905-666A-95
Sequence 90, App	10	US-09-905-666A-90
Sequence 93, App	10	US-09-905-666A-93
Sequence 56, App	10	US-09-905-666A-56
Sequence 92, App	10	US-09-905-666A-92
Sequence 70, App	10	US-09-905-666A-70
Sequence 68, App	10	US-09-905-666A-68

ALIGNMENTS

RESULT 1	US-09-905-666A-75	;	SEQUENCE 75, Application US/0905666A
		;	SEQUENCE 75, Application US/0905666A
		;	GENERAL INFORMATION:
		;	Publication No.: US0030096300A1
		;	APPLICANT: GIVER, LORRAINE J.
		;	MINSHILL, JEREMY
		;	APPLICANT: VOGEL, KURT
		;	TITLE OF INVENTION: NOVEL LIPOASE GENES
		;	FILE REFERENCE: 0184_310US
		;	CURRENT APPLICATION NUMBER: US/09/905-666A
		;	CURRENT FILING DATE: 2002-10-15
		;	PRIOR APPLICATION NUMBER: 60/211,954
		;	PRIOR FILING DATE: 2000-07-13
		;	PRIOR FILING DATE: 2001-06-21
		;	NUMBER OF SEQ ID NOS: 111
		;	SOFTWARE: Patentin Ver. 2.1
		;	SEQ ID NO: 75
		;	TYPE: PRT
		;	ORGANISM: Artificial Sequence
		;	FEATURE:
		;	OTHER INFORMATION: Description of Artificial Sequence: Synthetic
		;	;

RESULT 2
 Qy 121 KILYTISSADMIVMNLSKLDGAKNQIHDGVHIGLMMSQVNSLKEGLNGGLNTN 180
 Db 121 KILYTISSADMIVMNLSKLDGAKNQIHDGVHIGLMMSQVNSLKEGLNGGLNTN 180
 US-09-905-666A-104
 / Sequence 104, Application US/0905666A
 / Publication No. US20030096390A1
 / APPLICANT: GIVER, LORRAINE J.
 / APPLICANT: MINSHULL, JEREMY
 / APPLICANT: VOGEL, KURT
 / TITLE OF INVENTION: NOVEL LIPASE GENES
 / CURRENT APPLICATION NUMBER: US/09/905,666A
 / CURRENT FILING DATE: 2002-10-15
 / PRIOR APPLICATION NUMBER: 60/17,944
 / PRIOR FILING DATE: 2000-07-13
 / NUMBER OF SEQ ID NOS: 111
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE: Peptide
 / OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 / OTHER INFORMATION: Peptide
 US-09-905-666A-104

Query Match 98.7%; Score 927; DB 10; Length 180;
 Best Local Similarity 98.3%; Pred. No. 1.2e-91;
 Matches 177; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 EHNPPVMVHIGGASFNFAGIKSYLVSQWSRCKYAVDFTKTYNNGPVLSPRFVK 60
 Db 1 EHNPPVMVHIGGASFNFAGIKSYLVSQWSRCKYAVDFTKTYNNGPVLSPRFVK 60
 Qy 61 VLDETGAKYDIVAHSGGANTLYIKNDGKNIENVVTLGGANRSTSKALPDTDPRQ 120
 Db 61 VLDETGAKYDIVAHSGGANTLYIKNDGKNIENVVTLGGANRSTSKALPDTDPRQ 120
 Qy 121 KILYTISSADMIVMNLSKLDGAKNQIHDGVHIGLMMSQVNSLKEGLNGGLNTN 180
 Db 121 KILYTISSADMIVMNLSKLDGAKNQIHDGVHIGLMMSQVNSLKEGLNGGLNTN 180
 US-09-905-666A-78
 / Sequence 78, Application US/0905666A
 / Publication No. US20030096390A1
 / APPLICANT: GIVER, LORRAINE J.
 / APPLICANT: MINSHULL, JEREMY
 / APPLICANT: VOGEL, KURT
 / TITLE OF INVENTION: NOVEL LIPASE GENES
 / CURRENT APPLICATION NUMBER: US/09/905,666A
 / CURRENT FILING DATE: 2002-10-15
 / PRIOR APPLICATION NUMBER: 60/17,944
 / PRIOR FILING DATE: 2000-07-13
 / NUMBER OF SEQ ID NOS: 111
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE: Peptide
 / OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 / OTHER INFORMATION: Peptide
 US-09-905-666A-78

RESULT 4
 US-09-905-666A-98
 / Sequence 98, Application US/0905666A
 / Publication No. US20030096390A1
 / APPLICANT: GIVER, LORRAINE J.
 / APPLICANT: MINSHULL, JEREMY
 / APPLICANT: VOGEL, KURT
 / TITLE OF INVENTION: NOVEL LIPASE GENES
 / FILE REFERENCE: 0184:310US
 / CURRENT APPLICATION NUMBER: US/09/905,666A
 / CURRENT FILING DATE: 2002-10-15
 / PRIOR APPLICATION NUMBER: 60/217,954
 / PRIOR FILING DATE: 2000-07-13
 / PRIOR APPLICATION NUMBER: 60/300,378
 / PRIOR FILING DATE: 2001-06-21
 / SEQ ID NO: 98
 / LENGTH: 180
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE: Peptide
 / OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 / OTHER INFORMATION: Peptide
 US-09-905-666A-98

Query Match 98.4%; Score 924; DB 10; Length 180;
 Best Local Similarity 97.8%; Pred. No. 2.8e-91;
 Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 EHNPPVMVHIGGASFNFAGIKSYLVSQWSRCKYAVDFTKTYNNGPVLSPRFVK 60
 Db 1 EHNPPVMVHIGGASFNFAGIKSYLVSQWSRCKYAVDFTKTYNNGPVLSPRFVK 60
 Qy 61 VLDETGAKYDIVAHSGGANTLYIKNDGKNIENVVTLGGANRSTSKALPDTDPRQ 120
 Db 61 VLDETGAKYDIVAHSGGANTLYIKNDGKNIENVVTLGGANRSTSKALPDTDPRQ 120
 Qy 121 KILYTISSADMIVMNLSKLDGAKNQIHDGVHIGLMMSQVNSLKEGLNGGLNTN 180
 Db 121 KILYTISSADMIVMNLSKLDGAKNQIHDGVHIGLMMSQVNSLKEGLNGGLNTN 180
 US-09-905-666A-76
 / Sequence 76, Application US/0905666A
 / Publication No. US20030096390A1
 / APPLICANT: GIVER, LORRAINE J.
 / APPLICANT: MINSHULL, JEREMY
 / APPLICANT: VOGEL, KURT

TITLE OF INVENTION: NOVEL LIPASE GENES
 FILE REFERENCE: 0184_310US
 CURRENT FILING DATE: US/09/905, 666A
 PRIORITY APPLICATION NUMBER: 2002-10-15
 PRIORITY APPLICATION NUMBER: 60/217, 954
 PRIORITY FILING DATE: 2000-07-13
 PRIORITY FILING DATE: 60/300, 378
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 76
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-09-905-666A-76

Query Match 98.3%; Score 923; DB 10; Length 180;
 Best Local Similarity 97.8%; Pred. No. 3.2e-91;
 Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 EHNPPVVMHIGGASFNFAGIKSVLVSQGRGLYAYDFWDKTGTNYNNGPVLSREVKK 60
 Db 1 EHNPPVVMHIGGASFNFAGIKSVLVSQGRGLYAYDFWDKTGTNYNNGPVLSREVKK 60
 Qy 61 VLDETGAKKDVIAHSMGGANTLYYIKNLDGKNIKVNTVTLGCTNRSSTS KALPGTDPNQ 120
 Db 61 VLDTKGAKKDVIAHSMGGANTLYYIKNLDGKNIKVNTVTLGCTNRSSTS KALPGTDPNQ 120
 Qy 121 KILYTSYSSADMIVMANYLSKLDGAKNYQIHGVIGHI LIMNSQNSLIEKG LGG LNTN 180
 Db 121 KILYTSYSSADMIVMANYLSKLDGAKNYQIHGVIGHI LIMNSQNSLIEKG LGG LNTN 180

RESULT 6
 US-09-905-666A-108
 ; Sequence 108, Application US/0905666A
 ; Publication No. US20030096390A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GIVER, LORRAINE J.
 ; APPLICANT: VOGEL, KURT
 ; TITLE OF INVENTION: NOVEL LIPASE GENES
 ; FILE REFERENCE: 0184_310US
 ; CURRENT APPLICATION NUMBER: US/09/905, 666A
 ; CURRENT FILING DATE: 2000-10-15
 ; PRIORITY FILING DATE: 2000-07-13
 ; NUMBER OF SEQ ID NOS: 111
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 108
 ; LENGTH: 180
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 US-09-905-666A-108

Query Match 98.3%; Score 923; DB 10; Length 180;
 Best Local Similarity 97.8%; Pred. No. 3.2e-91;
 Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 EHNPPVVMHIGGASFNFAGIKSVLVSQGRGLYAYDFWDKTGTNYNNGPVLSREVKK 60
 Db 1 EHNPPVVMHIGGASFNFAGIKSVLVSQGRGLYAYDFWDKTGTNYNNGPVLSREVKK 60
 Qy 61 VLDETGAKKDVIAHSMGGANTLYYIKNLDGKNIKVNTVTLGCTNRSSTS KALPGTDPNQ 120
 Db 61 VLDETGAKKDVIAHSMGGANTLYYIKNLDGKNIKVNTVTLGCTNRSSTS KALPGTDPNQ 120
 Qy 121 KILYTSYSSADMIVMANYLSKLDGAKNYQIHGVIGHI LIMNSQNSLIEKG LGG LNTN 180
 Db 121 KILYTSYSSADMIVMANYLSKLDGAKNYQIHGVIGHI LIMNSQNSLIEKG LGG LNTN 180

RESULT 7
 US-09-905-666A-87
 ; Sequence 87, Application US/0905666A
 ; Publication No. US20030096390A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GIVER, LORRAINE J.
 ; APPLICANT: VOGEL, KURT
 ; TITLE OF INVENTION: NOVEL LIPASE GENES
 ; FILE REFERENCE: 0184_310US
 ; CURRENT APPLICATION NUMBER: US/09/905, 666A
 ; CURRENT FILING DATE: 2000-10-15
 ; PRIORITY FILING DATE: 2000-07-13
 ; NUMBER OF SEQ ID NOS: 111
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 87
 ; LENGTH: 180
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 US-09-905-666A-87

Query Match 98.2%; Score 922; DB 10; Length 180;
 Best Local Similarity 97.2%; Pred. No. 4.1e-91;
 Matches 175; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 EHNPPVVMHIGGASFNFAGIKSVLVSQGRGLYAYDFWDKTGTNYNNGPVLSREVKK 60
 Db 1 EHNPPVVMHIGGASFNFAGIKSVLVSQGRGLYAYDFWDKTGTNYNNGPVLSREVKK 60
 Qy 61 VLDETGAKKDVIAHSMGGANTLYYIKNLDGKNIKVNTVTLGCTNRSSTS KALPGTDPNQ 120
 Db 61 VLDETGAKKDVIAHSMGGANTLYYIKNLDGKNIKVNTVTLGCTNRSSTS KALPGTDPNQ 120
 Qy 121 KILYTSYSSADMIVMANYLSKLDGAKNYQIHGVIGHI LIMNSQNSLIEKG LGG LNTN 180
 Db 121 KILYTSYSSADMIVMANYLSKLDGAKNYQIHGVIGHI LIMNSQNSLIEKG LGG LNTN 180

RESULT 8
 US-09-905-666A-77
 ; Sequence 77, Application US/0905666A
 ; Publication No. US20030096390A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GIVER, LORRAINE J.
 ; APPLICANT: VOGEL, KURT
 ; TITLE OF INVENTION: NOVEL LIPASE GENES
 ; FILE REFERENCE: 0184_310US
 ; CURRENT APPLICATION NUMBER: US/09/905, 666A
 ; CURRENT FILING DATE: 2000-10-15
 ; PRIORITY FILING DATE: 2000-07-13
 ; NUMBER OF SEQ ID NOS: 111
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 77
 ; LENGTH: 180
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 US-09-905-666A-77

Query Match 98.3%; Score 923; DB 10; Length 180;
 Best Local Similarity 97.8%; Pred. No. 3.2e-91;
 Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 EHNPPVVMHIGGASFNFAGIKSVLVSQGRGLYAYDFWDKTGTNYNNGPVLSREVKK 60
 Db 1 EHNPPVVMHIGGASFNFAGIKSVLVSQGRGLYAYDFWDKTGTNYNNGPVLSREVKK 60
 Qy 61 VLDETGAKKDVIAHSMGGANTLYYIKNLDGKNIKVNTVTLGCTNRSSTS KALPGTDPNQ 120

```

FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; JS-09-905-666A-77

Query Match 98.0%; Score 920; DB 10; Length 180;
Best Local Similarity 91.2%; Pred. No. 6.8e-91;
Matches 175; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EHNPVVMYHIGGASFNFAKTSVLSQGMSRGKLYAEDFWDKGTYNNYNGPVLRSFVKK 60
  1 EHNPVVMYHIGGASFNFAKTSVLSQGMSRGKLYAEDFWDKGTYNNYNGPVLRSFVKK 60
Ddb 61 VLDDEGAKKVDIVAHSMGGANTLYIKNLDDGNNKVENVVTLGGTNRSTSKALPGTDPNQ 120
  61 VLDDEGAKKVDIVAHSMGGANTLYIKNLDDGNNKVENVVTLGGTNRSTSKALPGTDPNQ 120
Qy 121 KILVTSIYSSADMIVNNYVSKLDGAKNVQTHGVGHGILLMNQSONSLIKEGLNGGILNTN 180
  121 KILVTSIYSSADMIVNNYVSKLDGAKNVQTHGVGHGILLMNQSONSLIKEGLNGGILNTN 180
Ddb

RESULT 9
US-09-905-666A-58
Sequence 58, Application US/09905666A
; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184-310US
; CURRENT APPLICATION NUMBER: US/09/905, 666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217, 954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300, 378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Bacillus lentus
; JS-09-905-666A-58

```

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CURRENT APPLICATION NUMBER: US/09/905,666A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/217,954
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/300,378
PRIOR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO: 59
LENGTH: 212
TYPE: PRT
ORGANISM: Bacillus circulans
US-09-905-666A-59

Query Match 98.0%; Score 920;
Best Local Similarity 97.2%; Pred. No. 8
Matches 175; Conservative 3; Mismatch 1

Qy 1 EHNPNVWVHGTTGGASPNFGIGKSYLVSGQWSI
Db 33 EHNPNVWVHGTTGGASYNFGIGKSYLVSGQWSI

Qy 61 VLDETGAKKVDIVAHSMGGANTLYIKNLGDG
Db 93 VLDETGAKKVDIVAHSMGGANTLYIKNLGDGG

Qy 121 KLYTISIYSSADMIVMNYLSKLDGAKNQIHK
Db 153 KLYTISIYSSADMIVMNYLSKLDGAKNQIHK

RESULT 11
US-10-028-247-4
; Sequence 4, Application US/10028247
; Publication No. US20020150594A1
; GENERAL INFORMATION:
; APPLICANT: Goldman, Stanley
; APPLICANT: Lathrop, Stephanie J.
; APPLICANT: Longchamp, Pascal F.
; APPLICANT: Whalen, Robert G.
; APPLICANT: Maxygen, Inc.
; TITLE OF INVENTION: Methods and Composition
; TITLE OF INVENTION: Systems for Medicinal
; FILE REFERENCE: 18079-0332120US
; CURRENT APPLICATION NUMBER: US/110/028,247
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US/09/892,208
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US/09/892,208
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO: 4
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Bacillus circulans
; FEATURE:
; OTHER INFORMATION: lipase 396
US-10-028-247-4

Query Match 98.0%; Score 920;
Best Local Similarity 97.2%; Pred. No. 8
Matches 175; Conservative 3; Mismatch 1

Qy 1 EHNPNVWVHGTTGGASPNFGIGKSYLVSGQWSI
Db 33 EHNPNVWVHGTTGGASYNFGIGKSYLVSGQWSI

Qy 61 VLDETGAKKVDIVAHSMGGANTLYIKNLGDG
Db 93 VLDETGAKKVDIVAHSMGGANTLYIKNLGDGG

Qy 121 KLYTISIYSSADMIVMNYLSKLDGAKNQIHK

```

RESULT 12
 US-09-905-666A-99
 Sequence 99, Application US/0905666A
 Publication No. US20030096390A1
 GENERAL INFORMATION:
 APPLICANT: GIVER, LORRAINE J.
 APPLICANT: MINSHULL, JEREMY
 APPLICANT: VOEGEL, KURT
 TITLE OF INVENTION: NOVEL LIASE GENES
 FILE REFERENCE: 0184-310US
 CURRENT APPLICATION NUMBER: US/09/905,666A
 CURRENT FILING DATE: 2002-10-15
 PRIOR APPLICATION NUMBER: 60/217,954
 PRIOR FILING DATE: 2000-07-13
 PRIOR APPLICATION NUMBER: 60/300,378
 PRIOR FILING DATE: 2001-06-21
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 99
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-09-905-666A-99

Query Match 97.9%; Score 919; DB 10; Length 180;
 Best Local Similarity 97.2%; Pred. No. 8 7e-91;
 Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EHNPPVMMHIGGASFNAGIKSYLVSQWSRGKLYAIDFWDTGTNYNGPVLSRFKK 60
 Db 1 EHNPPVMMHIGGASFNAGIKSYLVSQWSRGKLYAIDFWDTGTNYNGPVLSRFKK 60
 Qy 61 VLDEGAKKVDIVAHSMGGANTLYKNDGGNKVENTYLGGTNRSTTSKALPGTDPNQ 120
 Db 61 VLDEGAKKVDIVAHSMGGANTLYKNDGGNKVENTYLGGTNRSTTSKALPGTDPNQ 120
 Qy 121 KILYTSIYSSADMIVNLYSLKDGAKVQTHGVIGHILMNSQNSLKEGLNGGLNTN 180
 Db 121 KILYTSIYSSADMIVNLYSLKDGAKVQTHGVIGHILMNSQNSLKEGLNGGLNTN 180

RESULT 13
 US-09-905-666A-82
 Sequence 82, Application US/0905666A
 Publication No. US20030096390A1
 GENERAL INFORMATION:
 APPLICANT: GIVER, LORRAINE J.
 APPLICANT: MINSHULL, JEREMY
 APPLICANT: VOEGEL, KURT
 TITLE OF INVENTION: NOVEL LIASE GENES
 FILE REFERENCE: 0184-310US
 CURRENT APPLICATION NUMBER: US/09/905,666A
 CURRENT FILING DATE: 2002-10-15
 PRIOR APPLICATION NUMBER: 60/217,954
 PRIOR FILING DATE: 2000-07-13
 PRIOR APPLICATION NUMBER: 60/300,378
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 82
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide

RESULT 14
 US-09-905-666A-107
 Sequence 107, Application US/0905666A
 Publication No. US20030096390A1
 GENERAL INFORMATION:
 APPLICANT: GIVER, LORRAINE J.
 APPLICANT: MINSHULL, JEREMY
 APPLICANT: VOEGEL, KURT
 TITLE OF INVENTION: NOVEL LIASE GENES
 FILE REFERENCE: 0184-310US
 CURRENT APPLICATION NUMBER: US/09/905,666A
 CURRENT FILING DATE: 2002-10-15
 PRIOR APPLICATION NUMBER: 60/217,954
 PRIOR FILING DATE: 2000-07-13
 PRIOR APPLICATION NUMBER: 60/300,378
 PRIOR FILING DATE: 2001-06-21
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 107
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-09-905-666A-107

Query Match 97.7%; Score 917; DB 10; Length 180;
 Best Local Similarity 97.8%; Pred. No. 1 4e-90;
 Matches 176; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EHNPPVMMHIGGASFNAGIKSYLVSQWSRGKLYAIDFWDTGTNYNGPVLSRFKK 60
 Db 1 EHNPPVMMHIGGASFNAGIKSYLVSQWSRGKLYAIDFWDTGTNYNGPVLSRFKK 60
 Qy 61 VLDEGAKKVDIVAHSMGGANTLYKNDGGNKVENTYLGGTNRSTTSKALPGTDPNQ 120
 Db 61 VLDEGAKKVDIVAHSMGGANTLYKNDGGNKVENTYLGGTNRSTTSKALPGTDPNQ 120
 Qy 121 KILYTSIYSSADMIVNLYSLKDGAKVQTHGVIGHILMNSQNSLKEGLNGGLNTN 180
 Db 121 KILYTSIYSSADMIVNLYSLKDGAKVQTHGVIGHILMNSQNSLKEGLNGGLNTN 180

RESULT 15
 US-09-905-666A-102
 Sequence 102, Application US/0905666A
 Publication No. US20030096390A1
 GENERAL INFORMATION:
 APPLICANT: GIVER, LORRAINE J.
 APPLICANT: MINSHULL, JEREMY
 APPLICANT: VOEGEL, KURT
 TITLE OF INVENTION: NOVEL LIASE GENES
 FILE REFERENCE: 0184-310US
 CURRENT APPLICATION NUMBER: US/09/905,666A
 CURRENT FILING DATE: 2002-10-15
 PRIOR APPLICATION NUMBER: 60/217,954
 PRIOR FILING DATE: 2000-07-13
 PRIOR APPLICATION NUMBER: 60/300,378
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 82
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide

CURRENT APPLICATION NUMBER: US/09/905,666A
 CURRENT FILING DATE: 2002-10-15
 PRIOR APPLICATION NUMBER: 60/17,954
 PRIOR FILING DATE: 2000-07-13
 PRIOR APPLICATION NUMBER: 60/300,378
 PRIOR FILING DATE: 2001-06-21
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 102
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-09-905-666A-102

Query Match 97.3%; Score 914; DB 10; Length 180;
 Best Local Similarity 96.7%; Pred. No. 3e-90; 0; Gaps 0;
 Matches 1174; Conservative 3; Mismatches 3; Indels 0;

Qy	1	EHNPVPMVYIGGASENPAGIKSYLVSOGWSRGKLYAVDFDVKTGTNYNNGPVLSPRFVKK	60
Db	1	EHNPVPMVYIGGASENPAGIKSYLVSOGWSRGKLYAVDFDVKTGTNYNNGPVLSPRFVKK	60
Qy	61	VLDETGAKRVDIVAHSMGCAANTYYINQIDGGMKVENVVTLGGTNRSTTSKALPDTDPO	120
Db	61	VLDETGAKRVDIVAHSMGCAANTYYINQIDGGMKVENVVTLGGTNRSTTSKALPDTDPO	120
Qy	121	KILYTSIYSSADMIVMNTLSKLDGAKRVOIHYGHTGLLMSQVNSLIKESLNGGGLNN	180
Db	121	KILYTSVYSSADMIVMNTLSKLDGAKRVOIHYGHTGLLMSQVNSLIKESLNGGQNTN	180

Search completed: April 23, 2004, 10:23:29
 Job time : 36.3571 secs

GenCore version 5.1.6
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OM protein - protein Search, using SW model

Run on: April 23, 2004, 10:08:37 ; Search time 15:1531 seconds
(without alignments)

613.254 Million cell updates/sec

Title: US-09-905-666A-75

Percent score: 93.9

Sequence: 1 EHNPPVMMHGIGGASFNFAG.....NSQVNNSIKEGLNGGGLNTN 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/2/iaa/5B_COMBO.PEP:*

3: /cgn2_6/ptodata/2/iaa/6A_COMBO.PEP:*

4: /cgn2_6/ptodata/2/iaa/6B_COMBO.PEP:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMBO.PEP:*

6: /cgn2_6/ptodata/2/iaa/backFiles1.PEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	74.7	79.6	213	1 US-07-330-678-2	Sequence 2, Appli
2	129.5	13.8	358	1 US-08-034-650-10	Sequence 10, Appli
3	129.5	13.8	358	1 US-08-419-015-10	Sequence 10, Appli
4	117.5	12.5	363	3 US-08-978-682A-2	Sequence 2, Appli
5	117.5	12.5	363	3 US-09-336-605-1	Sequence 1, Appli
6	117.5	12.5	363	4 US-09-219-120-2	Sequence 2, Appli
7	110.5	11.8	296	4 US-09-543-682A-7771	Sequence 7771, Appli
8	110.5	11.8	364	1 US-08-00-422-3	Sequence 3, Appli
9	110.0	11.7	351	4 US-09-252-991A-27337	Sequence 27337, Appli
10	107.5	11.4	318	4 US-09-189-03A-418	Sequence 418, Appli
11	97.5	10.4	690	4 US-09-134-001C-4168	Sequence 4568, Appli
12	95.5	10.2	699	4 US-09-134-001C-4054	Sequence 4054, Appli
13	94.5	10.1	299	4 US-09-584-568C-6	Sequence 6, Appli
14	93.5	10.0	292	4 US-19-134-001C-3301	Sequence 3301, Appli
15	92.5	9.9	308	4 US-09-584-568C-8	Sequence 8, Appli
16	92	9.8	316	4 US-09-107-512A-4594	Sequence 4594, Appli
17	90.5	9.6	325	4 US-09-328-332-6196	Sequence 6196, Appli
18	87.5	9.3	1216	4 US-09-134-000C-5130	Sequence 5130, Appli
19	86.5	9.2	388	1 US-08-32-519-2	Sequence 2, Appli
20	86.5	9.2	388	1 US-08-456-956-2	Sequence 2, Appli
21	85	9.2	264	4 US-09-134-001C-5592	Sequence 5592, Appli
22	85	9.2	1053	4 US-09-062-126-10	Sequence 10, Appli
23	85.5	9.1	453	4 US-09-328-332-5069	Sequence 5069, Appli
24	85	9.1	652	4 US-09-134-001C-3517	Sequence 3517, Appli
25	84.5	9.0	416	4 US-09-419-039A-8245	Sequence 8245, Appli
26	84	8.9	262	2 US-08-602-358A-35	Sequence 35, Appli
27	83.5	8.9	315	4 US-09-584-568C-2	Sequence 2, Appli

RESULT 1
US-07-930-678-2
; Sequence 2, Application US/07930678
; Patent No. 547936
; GENERAL INFORMATION:
; APPLICANT: MOELLER, Bernhard
; APPLICANT: WILKE, Detlef
; APPLICANT: FOUILLOIS, Bertrand
; TITLE OF INVENTION: Alkaline Bacillus Lipases Coding DNA
; Sequence Therefor and Bactilli, Which Produce These
; Lipases
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEES: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07-930,678
; FILING DATE: 1999/10/13
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/BP91/00664
; APPLICATION NUMBER: PCT/BP91/00664
; FILING DATE: 08/APR/1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 12 070 8
; FILING DATE: 14-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, J.D.
; REGISTRATION NUMBER: 26,269
; REPERENCE/DOCKET NUMBER: 16877/318/KACH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-3300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-930-678-2

ALIGNMENTS

NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
 STREET: P.O. BOX 747
 CITY: FALLS CHURCH
 STATE: VIRGINIA
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 22240
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/978,589A
 FILING DATE: 26-NOV-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 20-4336P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 363 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-978-589A-2

Query Match 12.5%; Score 117.5; DB 3; Length 363;
 Best Local Similarity 29.8%; Pred. No. 0.0002;
 Matches 39; Conservative 21; Mismatches 46; Indels 25; Gaps 8;

Qy 4 PVMVHGIGGASFNPIAGIKSYLVSGWSR-----GKLYAVD---FWDKTGTNTNG 51
 Db 54 PILLVHGLTGTID-KYGGVVEY----WYRIPEDLAHGANVYVANLSGFQSDDPN-GRG 106

Qy 52 PVLRSREVKKVLDGAKKVDIVAHGSMGGANTLYYYKNDGNGKTYENVVTLG---GTNRS 107
 Db 107 EQLLAFVQVLAATGQKVNLIGHSGQGL-TSRYVASV-APELVAVSVTTISTPHWGSQFA 164

Qy 108 TTISKALPGTDP 118
 Db 165 DFVQQLQTDP 175

Best Local Similarity 29.8%; Pred. No. 0.0002; Mismatches 46; Indels 25; Gaps 8;
 Matches 39; Conservative 21; Mismatches 46; Indels 25; Gaps 8;

RESULT 6
 US-09-219-120-2
 ; Sequence 2, Application US/09219120
 ; Patent No. 6472189
 ; GENERAL INFORMATION:
 ; APPLICANT: TAKESHI, Ishii
 ; APPLICANT: SATOSHI, Mitsu
 ; TITLE OF INVENTION: ESTERASE GENE AND ITS USE
 ; FILE REFERENCE: 20-4336P
 ; CURRENT APPLICATION NUMBER: US/09/219,120
 ; CURRENT FILING DATE: 1998-12-23
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 363
 ; TYPE: PRT
 ; ORGANISM: Burkholderia cepacia

Query Match 12.5%; Score 117.5; DB 4; Length 363;
 Best Local Similarity 29.8%; Pred. No. 0.0002;
 Matches 39; Conservative 21; Mismatches 46; Indels 25; Gaps 8;

Qy 4 PVMVHGIGGASFNPIAGIKSYLVSGWSR-----GKLYAVD---FWDKTGTNTNG 51
 Db 54 PILLVHGLTGTID-KYGGVVEY----WYRIPEDLAHGANVYVANLSGFQSDDPN-GRG 106

Qy 52 PVLRSREVKKVLDGAKKVDIVAHGSMGGANTLYYYKNDGNGKTYENVVTLG---GTNRS 107
 Db 107 EQLLAFVQVLAATGQKVNLIGHSGQGL-TSRYVASV-APELVAVSVTTISTPHWGSQFA 164

Qy 108 TTISKALPGTDP 118
 Db 165 DFVQQLQTDP 175

RESULT 7
 US-09-543-681A-7771
 ; Sequence 771, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; FILE REFERENCE: 2709-1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 7771
 ; LENGTH: 296
 ; TYPE: PRT
 ; ORGANISM: Proteus mirabilis

Query Match 11.8%; Score 110.5; DB 4; Length 296;

Best Local Similarity 31.6%; Pred. No. 0.00085; Matches 36; Conservative 15; Mismatches 44; Indels 19; Gaps 5;

Qy 4 PYVMVHGIGGASFN-----PAGIKSYLSQGWS-RGGLYAYDFWDKTKTNYNNGPWL 54
Db 15 PIVLVLHGLG-FNEITVGFPIFYGFADALRQDHQFVTAISAFN-----SNEVRGFIOL 66

Qy 55 SRFVKVLDTEGAKKVDIVASMGANTLYIKNLGGNVENTVTLGGTNRST 108
Db 67 WQFVOTLQETQAKKVNFGTQSGPLACRVAANTP--DEVASATTSINSVNHGS 118

RESULT 8
US-08-400-422-3
; Sequence 3, Application US/08400422
; GENERAL INFORMATION:
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Diderichsen, Boerge Krag
; APPLICANT: Buckley, Catherine M.
; APPLICANT: Hobson, Audrey
; APPLICANT: McConell, David J.
; TITLE OF INVENTION: A process for the preparation of an active
; TITLE OF INVENTION: Lipase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56817150 No. 5681715disk of No. 5681715th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,422
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/038,763
FILING DATE: 25-MAR-1993
APPLICATION NUMBER: PCT/DK91/00402
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00391
FILING DATE: 18-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 32,728
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Pseudomonas cepacia
STRAIN: DSM 3401

Matches 35; Conservative 16; Mismatches 45; Indels 17; Gaps 6;

Qy 4 PYVMVHGIGGASFNAGIKSY-----IVSQGWRSRGKLYAYDFWDKTKTNYNNGPV 53
Db 54 PIVLVLHGLG-FNEITVGFPIFYGFADALRQDHQFVTAISAFN-----SNEVRGFIOL 66

Qy 54 LSRFVKVLDTEGAKKVDIVASMGANTLYIKNLGGNVENTVTLGGTNR 106
Db 109 LIAYVKTFLAATGATKVNLVGHXQGJLTSRVVA--AVAPDLIVASVTIGPFR 159

RESULT 9
US-09-252-991A-27337
; Sequence 27337, Application US/09252991A
; GENERAL INFORMATION:
; Patent No. 6551795
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27337
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27337

Query Match 11.7%; Score 110; DB 4; Length 351;
Best Local Similarity 25.3%; Pred. No. 0.0012; Mismatches 54; Indels 40; Gaps 7;

Qy 4 PYVMVHGIGGASFNAGIKSYIVSQGWRSRGKLYAYDFWDKTKTNYNNGPV 53
Db 75 PIVLVLHGLG-FNEITVGFPIFYGFADALRQDHQFVTAISAFN-----DVKTG----- 45

Qy 46 -IVNNGDVLISRFVKVLDTEGAKKVDIVASMGANTLYIKNLGGNVENTVTLGGT 104
Db 117 NSNEVRBQLLAQVEVTLGAEKVNLLGHSGQEN-TVRYVAGV-APQLYAVSFTMGT 174

Qy 105 NRST-TSKALPDTDPNKLIVTSIVSSADMVNTLSKLDGARNVQ 149
Db 175 HUGTPVDAVTSFSEFZGPICIEVAVAEFLSVDIVDGWV 220

RESULT 10
US-09-489-039A-7418
; Sequence 7418, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7418
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7418

Query Match 11.4%; Score 107.5; DB 4; Length 318;
Best Local Similarity 26.9%; Pred. No. 0.002; Mismatches 30; Indels 31; Gaps 8;

Query Match 11.8%; Score 110.5; DB 1; Length 364;
Best Local Similarity 31.0%; Pred. No. 0.001; Mismatches 30; Indels 31; Gaps 8;

US-08-400-422-3

RESULT 11

Query 5 VVNVHGIG-GAS- FNPAIGIKSYLVSQGWGRGKLYAYDFWDKGITGNYNNG--- PVLSRFFV 58
 SEQ ID NO: 4054
 LENGTH: 699
 TYPE: PRT
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-4054

Query 68 VMLHGSSP-GATGWAESRNRDPLVEAGY-RVLLDCPGKKSDAIVNSRSRDLNARIL 126
 Best Local Similarity 22.7%; Pred. No. 0.13%; Length 699;
 Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

Query 59 KKVLDETGAKYKDIVAHSGGANTLYIKNLDGGKVNENVTLLGG-----TNR 106
 Best Local Similarity 22.7%; Pred. No. 0.13%; Length 699;
 Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

Query 127 KSVVDQLDGIDRTHLGNMGHSAVAF-TLSWPERVAKVLMGGTGGMSLFTPMP?EG 184
 Best Local Similarity 22.7%; Pred. No. 0.13%; Length 699;
 Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

Query 107 STISKAL---PCTDPNOKILTYSISSADM1-----VNNYLSKLDGAKN 147
 Best Local Similarity 22.7%; Pred. No. 0.13%; Length 699;
 Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

Query 185 IKULNLYREPTENLKKMMSITFVFDTRDLEALFARINMMLSRDHLDN 235
 Best Local Similarity 22.7%; Pred. No. 0.13%; Length 699;
 Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

RESULT 12

Query 1 Sequence 4568, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 FILE REFERENCE: GIC-007
 CURRENT APPLICATION NUMBER: US 09/134.001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064, 964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055, 779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO: 4568
 LENGTH: 690
 TYPE: PRT
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-4568

Query 2 VVNVHGIG-GAS- FNPAIGIKSYLVSQGWGRGKLYAYDFWDKGITGNYNNG--- PVLSRFFV 58
 Best Local Similarity 22.5%; Pred. No. 0.075%; Length 690;
 Matches 50; Conservative 25; Mismatches 60; Indels 87; Gaps 10;

Query 4 VVNVHGIG-GAS- FNPAIGIKSYLVSQGWGRGKLYAYDFWDKGITGNYNNG--- PVLSRFFV 58
 Best Local Similarity 22.5%; Pred. No. 0.075%; Length 690;
 Matches 50; Conservative 25; Mismatches 60; Indels 87; Gaps 10;

Query 310 PVVFVHGIG-G---FASDNOFLSLAPKXWGGKXNTDRNLTNEGTVHEANIGAF---SS 361
 Best Local Similarity 22.5%; Pred. No. 0.075%; Length 690;
 Matches 50; Conservative 25; Mismatches 60; Indels 87; Gaps 10;

Query 47 NYNNGPVL-SRFLVKGKVLDEGA-----FKVDAVASHMGAN 81
 Best Local Similarity 22.5%; Pred. No. 0.075%; Length 690;
 Matches 50; Conservative 25; Mismatches 60; Indels 87; Gaps 10;

Query 362 NYDRAVEYYTKGRDYGAHAAKYGHRYGRTYKGIMRDWEPGKTHFIGHSMGGQT 421
 Best Local Similarity 22.5%; Pred. No. 0.075%; Length 690;
 Matches 50; Conservative 25; Mismatches 60; Indels 87; Gaps 10;

Query 82 TLY---TNR-----LIGG---NKVENVVTUGGTRNTRSTSKALPDT 117
 Best Local Similarity 22.5%; Pred. No. 0.075%; Length 690;
 Matches 50; Conservative 25; Mismatches 60; Indels 87; Gaps 10;

Query 422 IRQMEEFRLRNQOEIEYQRQHGGTISDLTGGKDNMVASITLTGTPHNGTPAADKGIT- 480
 Best Local Similarity 22.5%; Pred. No. 0.075%; Length 690;
 Matches 50; Conservative 25; Mismatches 60; Indels 87; Gaps 10;

Query 118 PNOKILTYSISSADM1VMTNLSKLDGAKNQIH-GVGHIGL 158
 Best Local Similarity 22.5%; Pred. No. 0.075%; Length 690;
 Matches 50; Conservative 25; Mismatches 60; Indels 87; Gaps 10;

Query 481 -RKLVRETI-----NRIGRLGGKGDVDIDGFSQNL 511
 Best Local Similarity 22.5%; Pred. No. 0.075%; Length 690;
 Matches 50; Conservative 25; Mismatches 60; Indels 87; Gaps 10;

RESULT 13

Query 3 NPVVMVHGIG-GAS- FNPAIGIKSYLVSQGWGRGKLYAYDFWDKGITGNYNNGP 62
 Best Local Similarity 22.7%; Pred. No. 0.13%; Length 699;
 Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

Query 338 NPSVTHYMGDRDN---IRQDLBENGAYEASIA---GSNYDRAVEYYIKGGR 390
 Best Local Similarity 22.7%; Pred. No. 0.13%; Length 699;
 Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

Query 63 DETGA-----KKYDIVAHSMGGANTLYIKNL-----89
 Best Local Similarity 22.7%; Pred. No. 0.13%; Length 699;
 Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

Query 391 VDYGAAHAAKYGHERGYGKTYEGVYKDWKPGQKTHLVGHSMSGG-QTIREEELLRHGNEE 449
 Best Local Similarity 22.7%; Pred. No. 0.13%; Length 699;
 Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

Query 90 -----DGG---NKVENVVTUGGTRNTRSTSKALPDTDPNOKILTYSISSAD 132
 Best Local Similarity 22.7%; Pred. No. 0.13%; Length 699;
 Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

Query 450 VEYQKQHGGGRISPLFQGGHDNMNSITLTGTPHNGTHASDUG---NEAVIRQLAYD--- 503
 Best Local Similarity 22.7%; Pred. No. 0.13%; Length 699;
 Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

Query 133 MIVDNLYSKLDGAKNQI-HGVGHIGL 158
 Best Local Similarity 22.7%; Pred. No. 0.13%; Length 699;
 Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

Query 504 -----VGRMYGNKNDSDRVDGLEWGL 524
 Best Local Similarity 22.7%; Pred. No. 0.13%; Length 699;
 Matches 47; Conservative 27; Mismatches 62; Indels 71; Gaps 9;

RESULT 14

Query 1 Sequence 6, Application US/09584568C-6
 Patent No. 6500657
 GENERAL INFORMATION:
 APPLICANT: Glucksmann, Maria, Alexandra et al
 TITLE OF INVENTION: 3316, A NOVEL HUMAN HYDROLASE AND USES THEREFOR
 FILE REFERENCE: MN1-140
 CURRENT APPLICATION NUMBER: US/09/584-568C
 CURRENT FILING DATE: 2000-05-31
 PRIOR APPLICATION NUMBER: 60/193, 954
 PRIOR FILING DATE: 2000-03-31
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 6
 LENGTH: 299
 TYPE: PRT
 ORGANISM: Caenorhabditis elegans
 US-09-584-568C-6

Query 2 HNPVVMVHGIG-GAS- FNPAIGIKSYLVSQGWGRGKLYAYDFWDKGITGNYNNGP----- 52
 Best Local Similarity 21.5%; Pred. No. 0.047%; Length 299;
 Matches 27; Conservative 24; Mismatches 40; Indels 19; Gaps 3;

Query 45 NSPLVIVHGFGLGQONNNNSVKGALKHK---LEAPVYAVD----RNHGSSHTETNSY 97
 Best Local Similarity 21.5%; Pred. No. 0.047%; Length 299;
 Matches 27; Conservative 24; Mismatches 40; Indels 19; Gaps 3;

Query 53 ---VLSRFRYKVLDETGAKKDVIAHSMGGANTLYIKNLDGKVN 99
 Best Local Similarity 21.5%; Pred. No. 0.047%; Length 299;
 Matches 27; Conservative 24; Mismatches 40; Indels 19; Gaps 3;

Query 98 MAEDLVLFIDKVKBETKTRVNLIGHSMGGKIVMRALDSKWSDRLEKL 147
 Best Local Similarity 21.5%; Pred. No. 0.047%; Length 299;
 Matches 27; Conservative 24; Mismatches 40; Indels 19; Gaps 3;

RESULT 15

Query 1 Sequence 3301, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 FILE REFERENCE: GIC-007
 CURRENT APPLICATION NUMBER: US/09/134, 001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064, 964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055, 779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 US-09-134-001C-3301

Query 2 Sequence 3301, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 FILE REFERENCE: GIC-007
 CURRENT APPLICATION NUMBER: US/09/134, 001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064, 964
 PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO: 3301

LENGTH: 292
 TYPE: PRT
 ORGANISM: *Staphylococcus epidermidis*
 US-09-134-001C-3301

Query Match 10.0%; Score 93.5; DB 4; Length 292;
 Best Local Similarity 21.8%; Pred. No. 0.058; Gaps 8;
 Matches 43; Conservative 26; Mismatches 47; Indels 81; Gaps 8;
 SRGKLY-----A 37

Qy 6 VMVHGIGGASENFAGIKSYLVSQGW-----
 Db 52 LFLHGGGSSERS---ETFWYKQALNKNVTVNEVITARYSEGVKVFDKKLSEDAANPIVK 107

Qy 38 VDFWD-KTGNYNNNGPVLSPREVKKYLDETGAKYDIVAHSGGANTLYYKNDGGNKE 96

Db 108 VEFKDNRKGNPKENAYWIEKVLSQLKSQFPIQQPMFVGHSMGNISAFYMKNY----- 160

Qy 97 NVTLGSTNRSTTSKALPQGTDPNOKILYTYSTYSSADMIVNNYLSKLDGAKRNQVIGHGVSHI 156

Db 161 -----GDD-----RHFQD--KKEVNLAGVING 181

Qy 157 GILMNQVNSL1-XEG 171

Db 182 ILMNNEVNETIVDKQG 198

RESULT 15
 US-09-584-568-C-8 Application US/09584568C
 / Sequence 8, Application US/09584568C
 / Patent No. 6500657
 / GENERAL INFORMATION:
 / APPLICANT: Glucksmann, Maria, Alexandra et al.
 / TITLE OF INVENTION: 33467, A NOVEL HUMAN HYDROLASE AND USES THEREFOR
 / FILE REFERENCE: MN1-140
 / CURRENT APPLICATION NUMBER: US/09/584,568C
 / CURRENT FILING DATE: 2000-05-31
 / PRIOR APPLICATION NUMBER: 60/193,954
 / PRIOR FILING DATE: 2000-03-31
 / NUMBER OF SEQ ID NOS: 11
 / SEQ ID NO: 8
 / LENGTH: 308
 / TYPE: PRM
 / ORGANISM: *Drosophila melanogaster*
 US-09-584-568-C-8

Query Match 9.9%; Score 92.5; DB 4; Length 308;
 Best Local Similarity 26.4%; Pred. No. 0.08; Gaps 3;
 Matches 23; Conservative 23; Mismatches 36; Indels 5; Gaps 3;
 SRGKLY-----A 60

Qy 4 PVMVHGIGGASPNFAGIKSYLVSQGWRSRGLYAVD--FWDKTGTYNNNGPVLSPRFVK 60

Db 54 PLLTYHGGLESKQWRGSKALVTK-VSR-KVIAIDVNRHGESPHSSVHNSKAMSEDLR 111

Qy 61 VLDETGAKYDIVAHSMGEGANTLYYIK 87

Db 112 FMEQRSHPAAHCMSGMGRSMYFAR 138

Search completed: April 23, 2004, 10:14:40
 Job time : 16.1531 secs

Gencore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 10:01:12 ; Search time 46.3776 Seconds
(without alignments)
1096.620 Million cell updates/sec

Title: US-09-905-666A-75

Perfect score: 939

Sequence: 1 EHNPPVVMHGIGGASFNFAG.....NSQVNLSLIKEGINGGGLNTN 180

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing First 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqD1980s:*

2: geneseqD1990s:*

3: geneseqD2000s:*

4: geneseqD2001s:*

5: geneseqD2002s:*

6: geneseqD2003as:*

7: geneseqD2003bs:*

8: geneseqD2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	939	100.0	180	5 AAU83861	Aau83861 Bacillus
2	925	98.7	180	5 AAU83890	Aau83890 Bacillus
3	925	98.5	180	5 AAU83864	Aau83864 Bacillus
4	924	98.4	180	5 AAU83884	Aau83884 Bacillus
5	923	98.3	180	5 AAU83862	Aau83862 Bacillus
6	923	98.3	180	5 AAU83894	Aau83894 Bacillus
7	922	98.2	180	5 AAU83873	Aau83873 Bacillus
8	920	98.0	180	5 AAU83863	Aau83863 Bacillus
9	920	98.0	212	5 AAU83845	Aau83845 Bacillus
10	920	98.0	212	5 AAU83844	Aau83844 Bacillus
11	912	97.9	180	5 AAU83885	Aau83885 Bacillus
12	917	97.9	180	5 AAU83868	Aau83868 Bacillus
13	917	97.7	180	5 AAU83893	Aau83893 Bacillus
14	914	97.3	180	5 AAU83888	Aau83888 Bacillus
15	913	97.2	180	5 AAU83889	Aau83889 Bacillus
16	913	97.2	212	5 AAU83891	Aau83891 Bacillus
17	912	97.2	180	5 AAU83848	Aau83848 Bacillus
18	912	97.1	180	5 AAU83867	Aau83867 Bacillus
19	911	97.0	180	5 AAU83887	Aau83887 Bacillus
20	911	97.0	180	5 AAU83886	Aau83886 Bacillus
21	909	96.8	212	5 AAU83847	Aau83847 Bacillus
22	909	96.8	212	5 AAU83841	Aau83841 Bacillus
23	907	96.6	180	5 AAU83883	Aau83883 Bacillus
24	906	96.5	180	5 AAU83874	Aau83874 Bacillus
25	906	96.5	180	5 AAU83872	Aau83872 Bacillus

ALIGNMENTS

RESULT 1	
ID	AAU83861 standard; protein; 180 AA.
XX	
AC	AAU83861;
XX	
DT	08-MAY-2002 (first entry)
XX	
DE	Bacillus lipase polypeptide #21.
XX	
XX	Libase; Bacillus; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory; synthetic.
XX	
OS	OSynthetic.
XX	
PN	WO200206457-A2.
XX	
PD	24-JAN-2002.
XX	
PF	13-JUL-2001; 2001WO-US022160.
XX	
PR	13-JUL-2000; 2000US-0217954P.
XX	
PR	21-JUN-2001; 2001US-0300378P.
XX	
PA	(MAXY-) MAXYGEN INC.
XX	
PI	Giver LJ, Minshull J, Vogel K;
XX	
DR	WPI; 2002-171805/22.
DR	N-PSDB; ABK3839.
XX	
CC	The invention relates to new <i>Bacillus</i> lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other
CC	
CC	Claim 5; Page 141; 196pp; English.
CC	

agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase polypeptides of the invention.

Sequence 180 AA;

Query Match 98 %; Score 925; DB 5; Length 180;
Best Local Similarity 97.8%; Pred. No. 1.7e-85;
Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EHNPVYMHIGGGASFNAGIKSYLVSQMSRGKLYAIDFWDTGTNYNNGIVLSPRKK 60
Db 1 EHNPVYMHIGGGASFNAGIKSYLVSQMSRGKLYAIDFWDTGTNYNNGIVLSPRKK 60
Qy 61 VLDETGAKKDIVAHSMGGANTLYIKNLDGKVKENVTLGCTNRSSTS KALPGTDPNQ 120
Db 61 VLDETGAKKDIVAHSMGGANTLYIKNLDGKVKENVTLGCTNRSSTS KALPGTDPNQ 120
Qy 121 KILYTSIYSSADMIVNVLSKLDGAKNQVQHGVSHIGLIMNSQNSLKEIINGGINTN 180
Db 121 KILYTSIYSSADMIVNVLSKLDGAKNQVQHGVSHIGLIMNSQNSLKEIINGGINTN 180

RESULT 4

AAU83884
ID AAU83884 standard; protein; 180 AA.
XX
AC AAU83884;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #44.
XX
Li⁺pe; Bacillus; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory;
KW respiratory; gastrointestinal.
XX
Synthetic.
OS
PN WO200206457-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001WO-US022160.
XX
PR 13-JUL-2000; 2000US-0217954P.
PR 21-JUN-2001; 2001US-0300378P.
XX
(MAXY-) MAXYGEN INC.
PA
Giver LJ, Minshull J, Vogel K;
XX
WPI; 2002-171805/22.
DR
N-PSDB, ABK33862.

Nucleic acids encoding lipase enzymes which are useful as supplements in animal feeds, as agents of flavor modification and for treating Crohn's disease and celiac disease.
Claim 5; Page 144; 196pp; English.
XX
The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavor modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food

agents, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase polypeptides of the invention.

Sequence 180 AA;

Query Match 98.4%; Score 924; DB 5; Length 180;
Best Local Similarity 97.8%; Pred. No. 2.2e-85;
Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EHNVVVWTHIGGGASFNAGIKSYLVSQMSRGKLYAIDFWDTGTNYNNGIVLSPRKK 60
Db 1 EHNVVVWTHIGGGASFNAGIKSYLVSQMSRGKLYAIDFWDTGTNYNNGIVLSPRKK 60
Qy 61 VLDETGAKKDIVAHSMGGANTLYIKNLDGKVKENVTLGCTNRSSTS KALPGTDPNQ 120
Db 61 VLDETGAKKDIVAHSMGGANTLYIKNLDGKVKENVTLGCTNRSSTS KALPGTDPNQ 120
Qy 121 KILYTSIYSSADMIVNVLSKLDGAKNQVQHGVSHIGLIMNSQNSLKEIINGGINTN 180
Db 121 KILYTSIYSSADMIVNVLSKLDGAKNQVQHGVSHIGLIMNSQNSLKEIINGGINTN 180

RESULT 5

AAU83862
ID AAU83862 standard; protein; 180 AA.
XX
AC AAU83862;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #22.
XX
Li⁺pe; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory;
KW respiratory; gastrointestinal.
XX
Synthetic.
OS
PN WO200206457-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001WO-US022160.
XX
PR 13-JUL-2000; 2000US-0217954P.
PR 21-JUN-2001; 2001US-0300378P.
XX
(MAXY-) MAXYGEN INC.
PA
Giver LJ, Minshull J, Vogel K;
XX
WPI; 2002-171805/22.
DR
N-PSDB, ABK33862.

Nucleic acids encoding lipase enzymes which are useful as supplements in animal feeds, as agents of flavor modification and for treating Crohn's disease and celiac disease.
Claim 5; Page 141; 196pp; English.
XX
The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavor modification and fat modification in

CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents; They are also useful for treating Crohn's disease, Cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent *Bacillus* lipase
 CC polypeptides of the invention.

XX Sequence 180 AA;

Query Match 98.3%; Score 923; DB 5; Length 180;
 Best Local Similarity 97.8%; Pred. No. 2.7e-85; DB 5; Length 180;
 Matches 176; Conservative 2; Mismatches 0; Gaps 0;
 XX

Qy 1 EHNPPVMMVHGIGASFNFGIKSYLVSQWGRKLYADWDKGKNTNGPVLSPRFVK 60
 Db 1 EHNPPVMMVHGIGASFNFGIKSYLVSQWGRKLYADWDKGKNTNGPVLSPRFVK 60
 Qy 61 VLDETGAKKVDTIAHSGGANTLYKKNLDGNNKENVVTLGGTNRSTTSKALPGTDPNQ 120
 Db 61 VLDETGAKKVDTIAHSGGANTLYKKNLDGNNKENVVTLGGTNRSTTSKALPGTDPNQ 120
 Qy 121 KILYTSIYSSADMIVNLYSLKUDGAKNVQHVGVHGLLANSQNSLKEGLNGGGLNTN 180
 Db 121 KILYTSIYSSADMIVNLYSLKUDGAKNVQHVGVHGLLANSQNSLKEGLNGGGLNTN 180

RESULT 6

AAU83894
 ID AAU83894 standard; protein; 180 AA.
 AC AAU83894;

XX DT 08-MAY-2002 (first entry)

DE *Bacillus* lipase polypeptide #54.

KW Lipase; *Bacillus*; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; Gastrointestinal mal-absorption;
 KW Gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 OS Synthetic.

XX PN WO200202457-A2.

XX PD 24-JAN-2002.

XX PP 13-JUL-2001; 2001WO-US022160.

XX PR 13-JUL-2000; 2000US-0217954P.

XX PR 21-JUN-2001; 2001US-0300378P.

XX PA (MAXY-) MAXYGEN INC.

XX PI Giver LJ, Minshull J, Vogel K;

XX DR WPI: 2002-171805/22.

XX DR N-PSDB; ABK33872.

Nucleic acids encoding lipase enzymes which are useful as supplements in
 PT animal feeds, as agents of flavor modification and for treating Crohn's
 PT disease and celiac disease.
 PS Claim 5; Page 145-146; 196pp; English.

The invention relates to new *Bacillus* lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in

CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for canning/processing of leather and as cleaning
 CC agent. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent *Bacillus* lipase
 CC polypeptides of the invention.

XX Sequence 180 AA;

Query Match 98.3%; Score 923; DB 5; Length 180;
 Best Local Similarity 97.8%; Pred. No. 2.7e-85; DB 5; Length 180;
 Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EHNPPVMMVHGIGASFNFGIKSYLVSQWGRKLYADWDKGKNTNGPVLSPRFVK 60
 Db 1 EHNPPVMMVHGIGASFNFGIKSYLVSQWGRKLYADWDKGKNTNGPVLSPRFVK 60
 Qy 61 VLDETGAKKVDTIAHSGGANTLYKKNLDGNNKENVVTLGGTNRSTTSKALPGTDPNQ 120
 Db 61 VLDETGAKKVDTIAHSGGANTLYKKNLDGNNKENVVTLGGTNRSTTSKALPGTDPNQ 120
 Qy 121 KILYTSIYSSADMIVNLYSLKUDGAKNVQHVGVHGLLANSQNSLKEGLNGGGLNTN 180
 Db 121 KILYTSIYSSADMIVNLYSLKUDGAKNVQHVGVHGLLANSQNSLKEGLNGGGLNTN 180

RESULT 7

AAU83873
 ID AAU83873 standard; protein; 180 AA.
 XX AC AAU83873;

XX DT 08-MAY-2002 (first entry)

DE *Bacillus* lipase polypeptide #33.
 XX Lipase; *Bacillus*; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; Gastrointestinal mal-absorption;
 KW Gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 OS Synthetic.

XX PN WO200206457-A2.

XX PD 24-JAN-2002.

XX PP 13-JUL-2001; 2001WO-US022160.

XX PR 13-JUL-2000; 2000US-0217954P.

XX PR 21-JUN-2001; 2001US-0300378P.

XX PA (MAXY-) MAXYGEN INC.

XX PI Giver LJ, Minshull J, Vogel K;

XX DR WPI: 2002-171805/22.

XX DR N-PSDB; ABK33851.

Nucleic acids encoding lipase enzymes which are useful as supplements in
 PT animal feeds, as agents of flavor modification and for treating Crohn's
 PT disease and celiac disease.
 PS Claim 5; Page 143; 196pp; English.

The invention relates to new *Bacillus* lipase enzymes and the nucleic
 CC acids encoding them.

XX The invention relates to new *Bacillus* lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolyzing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent *Bacillus* lipase polypeptides of the invention.

XX

SQ Sequence 212 AA;

Query Match 98.0%; Score 920; DB 5; Length 212;
Best Local Similarity 97.2%; Pred. No. 6.4e-85;
Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EHNPPVMMVHIGGASFNPAIGKSYLVLSQWSRGRKLYAYDFWDTGTGTYNNGPEVLSRVEVK 60
Db 33 EHNPPVMMVHIGGASFNPAIGKSYLVLSQWSRGRKLYAYDFWDTGTGTYNNGPEVLSRVEVK 92

QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGGKENVVTLLGGTNRSTTSKALPGTDPNQ 120
Db 93 VLDETGAKKVDIVAHSMGGANTLYIKNLDGGKENVVTLLGGANRITTSKALPGTDPNQ 152

QY 121 KILTYSISSADMIVMNTLSKLDGAKNVQIHGIGLMMNSQVNSLIKEINGGGLNTN 180
Db 153 KILTYSISSADMIVMNTLSKLDGAKNVQIHGIGLMMNSQVNSLIKEINGGGLNTN 212

RESULT 10

AAU83844

ID AAU83844 standard; protein; 212 AA.

XX

AC AAU83844;

XX DT 08-MAY-2002 (first entry)

XX Bacillus lipase polypeptide #4.

DE XX
KW Lipase; *Bacillus*; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; enzyme; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory; gastrointestinal; synthetic.

XX OS *Bacillus lentsus*.

XX PN WO200206457-A2.

XX PD 24-JAN-2002.

XX PP 13-JUL-2001; 2001WO-US022160.

XX PR 13-JUL-2000; 2000US-0217954P.

XX PR 21-JUN-2001; 2001US-0300378P.

XX PA (MAXY-) MAXYGEN INC.

XX PI Giver LJ, Minshull J, Vogel K;

XX DR WPI; 2002-171805/22.

XX DR N-PSDB; ABK33822.

XX PT Nucleic acids encoding lipase enzymes which are useful as supplements in animal feeds, as agents of flavor modification and for treating Crohn's disease and celiac disease.

PS Claim 20; Page 138-139; 196pp; English.

XX The invention relates to new *Bacillus* lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolyzing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent *Bacillus* lipase polypeptides of the invention.

XX

SQ Sequence 212 AA;

Query Match 98.0%; Score 920; DB 5; Length 212;
Best Local Similarity 97.2%; Pred. No. 6.4e-85;
Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EHNPPVMMVHIGGASFNPAIGKSYLVLSQWSRGRKLYAYDFWDTGTGTYNNGPEVLSRVEVK 60
Db 33 EHNPPVMMVHIGGASFNPAIGKSYLVLSQWSRGRKLYAYDFWDTGTGTYNNGPEVLSRVEVK 92

QY 61 VLDETGAKKVDIVAHSMGGANTLYIKNLDGGKENVVTLLGGTNRSTTSKALPGTDPNQ 120
Db 93 VLDETGAKKVDIVAHSMGGANTLYIKNLDGGKENVVTLLGGANRITTSKALPGTDPNQ 152

QY 121 KILTYSISSADMIVMNTLSKLDGAKNVQIHGIGLMMNSQVNSLIKEINGGGLNTN 180
Db 153 KILTYSISSADMIVMNTLSKLDGAKNVQIHGIGLMMNSQVNSLIKEINGGGLNTN 212

RESULT 11

AAU8385

ID AAU8385 standard; protein; 180 AA.

XX

AC AAU8385;

XX DT 08-MAY-2002 (first entry)

XX Bacillus lipase polypeptide #45.

XX Lipase; *Bacillus*; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; enzyme; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory; gastrointestinal; synthetic.

XX OS *W0200206457-A2*.

XX DD 24-JAN-2002.

XX PP 13-JUL-2001; 2001WO-US022160.

XX PR 13-JUL-2000; 2000US-0217954P.

XX PR 21-JUN-2001; 2001US-0300378P.

XX PA (MAXY-) MAXYGEN INC.

XX PI Giver LJ, Minshull J, Vogel K;

XX DR WPI; 2002-171805/22.

XX DR N-PSDB; ABK33833.

XX PT Nucleic acids encoding lipase enzymes which are useful as supplements in animal feeds, as agents of flavor modification and for treating Crohn's disease and celiac disease.

XX Claim 5; Page 144; 195pp; English.
 XX
 PS The invention relates to new *Bacillus* lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent *Bacillus* lipase polypeptides of the invention.

XX Sequence 180 AA;
 XX Query Match 97.9%; Score 919; DB 5; Length 180;
 Best Local Similarity 97.2%; Pred. No. 7e-85;
 Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 EHNPNVVMVHGGASFNFAGIKSVLVSQMSRGKLYAVDFWDKTGTNYNNGPVLSRFVKK 60
 Db 1 EHNPNVVMVHGGASFNFAGIKSVLVSQMSRGKLYAVDFWDKTGTNYNNGPVLSRFVKK 60
 Qy 61 VLDENGAKKDIVAHSMGGANTLYKRNLDGGNKRVENTVLLGCTNRSTTSKALPGTDPNQ 120
 Db 61 VLDENGAKKDIVAHSMGGANTLYKRNLDGGNKRVENTVLLGCTNRSTTSKALPGTDPNQ 120
 Qy 121 KILITSIYSSADMIVANVYLSKLDGAKNQVHGHIGLIMNSQNSLIEKGINGGGLNTN 180
 Db 121 KILITSIYSSADMIVANVYLSKLDGAKNQVHGHIGLIMNSQNSLIEKGINGGGLNTN 180

RESULT 12
 AAU83868
 ID AAU83868 standard; protein; 180 AA.
 XX
 AC AAU83868;
 XX
 DT 08-MAY-2002 (first entry)
 DE *Bacillus* lipase polypeptide #28.

XX Lipase; *Bacillus*; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; Gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory; gastrointestinal.
 XX Synthetic.

OS
 XX WO200206457-A2.
 XX
 PD 24-JAN-2002.
 XX 13-JUL-2001; 2001WO-US022160.
 XX 13-JUL-2000; 2000US-0217954P.
 PR 21-JUN-2001; 2001US-0300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX Giver LJ, Minshull J, Vogel K;
 XX
 DR WPI; 2002-171805/22.
 DR N-PSDB; ABR33846.
 XX Nucleic acids encoding lipase enzymes which are useful as supplements in animal feeds, as agents of flavor modification and for treating Crohn's

PT disease and celiac disease.
 XX
 PS Claim 7; Page 142; 195pp; English.

CC The invention relates to new *Bacillus* lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of leather and as cleaning emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent *Bacillus* lipase polypeptides of the invention.

XX Sequence 180 AA;
 XX Query Match 97.7%; Score 917; DB 5; Length 180;
 Best Local Similarity 96.7%; Pred. No. 1.e-84;
 Matches 174; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 EHNPNVVMVHGGASFNFAGIKSVLVSQMSRGKLYAVDFWDKTGTNYNNGPVLSRFVKK 60
 Db 1 EHNPNVVMVHGGASFNFAGIKSVLVSQMSRGKLYAVDFWDKTGTNYNNGPVLSRFVKK 60
 Qy 61 VLDENGAKKDIVAHSMGGANTLYKRNLDGGNKRVENTVLLGCTNRSTTSKALPGTDPNQ 120
 Db 61 VLDENGAKKDIVAHSMGGANTLYKRNLDGGNKRVENTVLLGCTNRSTTSKALPGTDPNQ 120
 Qy 121 KILITSIYSSADMIVANVYLSKLDGAKNQVHGHIGLIMNSQNSLIEKGINGGGLNTN 180
 Db 121 KILITSIYSSADMIVANVYLSKLDGAKNQVHGHIGLIMNSQNSLIEKGINGGGLNTN 180

RESULT 13
 AAU83893
 ID AAU83893 standard; protein; 180 AA.
 XX
 AC AAU83893;
 XX
 DT 08-MAY-2002 (first entry)
 DE *Bacillus* lipase polypeptide #53.

XX Lipase; *Bacillus*; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; Gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory; gastrointestinal.
 XX Synthetic.

OS
 XX WO200206457-A2.
 XX
 PD 24-JAN-2002.
 XX 13-JUL-2001; 2001WO-US022160.
 XX 13-JUL-2000; 2000US-0217954P.
 PR 21-JUN-2001; 2001US-0300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX Giver LJ, Minshull J, Vogel K;
 XX
 DR WPI; 2002-171805/22.
 DR N-PSDB; ABR33871.

XX Nucleic acids encoding lipase enzymes which are useful as supplements in animal feeds, as agents of flavor modification and for treating Crohn's

PT disease and celiac disease.

animal feeds, as agents of flavor modification and for treating Crohn's disease and celiac disease.

Claim 5: Page 145; 196pp; English.

The invention relates to new *Bacillus* lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavor modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent *Bacillus* lipase polypeptides of the invention.

Sequence 180 AA;

Query Match	97.7%	Score	917	DB	5;	Length	180;
Best Local Similarity	97.8%	Pred. No.	1.1e-84;				
Matches	176;	Conservative	1;	Mismatches	3;	Indels	0;
						Gaps	0;
Qy	1	EEHNPVVMVHIGGASFNFGAKTSVLYSGRSRGKLYAIDFWDKTGTTGNYNNGPVLSRFYKK	60	Qy	1	EEHNPVVMVHIGGASFNFGAKTSVLYSGRSRGKLYAIDFWDKTGTTGNYNNGPVLSRFYKK	60
Db	1	EEHNPVVMVHIGGASFNFGAKTSVLYSGRSRGKLYAIDFWDKTGTTGNYNNGPVLSRFYKK	60	Db	1	EEHNPVVMVHIGGASFNFGAKTSVLYSGRSRGKLYAIDFWDKTGTTGNYNNGPVLSRFYKK	60
Qy	61	VLDETGAKKDIVAHSMGGANTLYKKNLDGGNKVENVVTLGGTNRSTSISKALPGTDNQ	120	Qy	61	VLDETGAKKDIVAHSMGGANTLYKKNLDGGNKVENVVTLGGTNRSTSISKALPGTDNQ	120
Db	61	VLDETGAKKDIVAHSMGGANTLYKKNLDGGNKVENVVTLGGTNRSTSISKALPGTDNQ	120	Db	61	VLDETGAKKDIVAHSMGGANTLYKKNLDGGNKVENVVTLGGTNRSTSISKALPGTDNQ	120
Qy	121	KILYTSIYSSADMIVNNYLSSLDGAKNVQIHGVGHIGLIMNSQVNSLIKEGLNGGQNTN	180	Qy	121	KILYTSIYSSADMIVNNYLSSLDGAKNVQIHGVGHIGLIMNSQVNSLIKEGLNGGQNTN	180
Db	121	KILYTSIYSSADMIVNNYLSSLDGAKNVQIHGVGHIGLIMNSQVNSLIKEGLNGGQNTN	180	Db	121	KILYTSIYSSADMIVNNYLSSLDGAKNVQIHGVGHIGLIMNSQVNSLIKEGLNGGQNTN	180

RESULT 14

AAU83888 standard; protein: 180 AA.

AAU83888;

08-MAY-2002 (first entry)

Bacillus lipase polypeptide #48.

XX Lipase; *Bacillus*; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory; gastrointestinal. XX Synthetic.

XX WO200206457-A2.

XX 24-JAN-2002.

XX 13-JUL-2001; 2001WO-US022160.

XX 13-JUL-2000; 2000US-0217954P.

PR 21-JUN-2001; 2001US-0300378P.

XX (MAXY-) MAXYGEN INC.

XX Giver LJ, Minshull J, Vogel K;

XX PR 13-JUL-2000; 2000US-0217954P.

PR 21-JUN-2001; 2001US-0300378P.

XX (MAXY-) MAXYGEN INC.

XX Giver LJ, Minshull J, Vogel K;

XX DR WPI; 2002-171805/22.

XX DR N-PSDB; ABK33867.

DR

Nucleic acids encoding lipase enzymes which are useful as supplements in animal feeds, as agents of flavor modification and for treating Crohn's disease and celiac disease.

PS

PS Claim 5; Page 145; 196pp; English.

PT The invention relates to new *Bacillus* lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in

PT animal feeds, as agents of flavor modification and fat modification in

PT human foodstuffs (e.g. cheese), as agents in the creation of food

PT emulsifiers, as agents for tanning/processing of leather and as cleaning

PT agents. They are also useful for treating Crohn's disease, cystic

PT fibrosis, coeliac disease, indigestion, obesity and other

PT gastrointestinal mal-absorption problems. Gastrointestinal lipid related

PT conditions can be therapeutically or prophylactically treated via a

PT method of hydrolysing a lipid comprising expressing in a target cell or

PT contacting a target cell with an effective amount of DNA or protein of

PT the invention. Sequences AAU83841-AAU83897 represent *Bacillus* lipase

PT polypeptides of the invention.

XX SQ Sequence 180 AA;

Query Match 97.7%; Score 917; DB 5; Length 180;
Best Local Similarity 97.8%; Pred. No. 1.1e-84;
Matches 176; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

XX Matches 174; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy	1	EEHNPVVMVHIGGASFNFGAKTSVLYSGRSRGKLYAIDFWDKTGTTGNYNNGPVLSRFYKK	60	Qy	1	EEHNPVVMVHIGGASFNFGAKTSVLYSGRSRGKLYAIDFWDKTGTTGNYNNGPVLSRFYKK	60
Db	1	EEHNPVVMVHIGGASFNFGAKTSVLYSGRSRGKLYAIDFWDKTGTTGNYNNGPVLSRFYKK	60	Db	1	EEHNPVVMVHIGGASFNFGAKTSVLYSGRSRGKLYAIDFWDKTGTTGNYNNGPVLSRFYKK	60
Qy	61	VLDETGAKKDIVAHSMGGANTLYKKNLDGGNKVENVVTLGGTNRSTSISKALPGTDNQ	120	Qy	61	VLDETGAKKDIVAHSMGGANTLYKKNLDGGNKVENVVTLGGTNRSTSISKALPGTDNQ	120
Db	61	VLDETGAKKDIVAHSMGGANTLYKKNLDGGNKVENVVTLGGTNRSTSISKALPGTDNQ	120	Db	61	VLDETGAKKDIVAHSMGGANTLYKKNLDGGNKVENVVTLGGTNRSTSISKALPGTDNQ	120
Qy	121	KILYTSIYSSADMIVNNYLSSLDGAKNVQIHGVGHIGLIMNSQVNSLIKEGLNGGQNTN	180	Qy	121	KILYTSIYSSADMIVNNYLSSLDGAKNVQIHGVGHIGLIMNSQVNSLIKEGLNGGQNTN	180
Db	121	KILYTSIYSSADMIVNNYLSSLDGAKNVQIHGVGHIGLIMNSQVNSLIKEGLNGGQNTN	180	Db	121	KILYTSIYSSADMIVNNYLSSLDGAKNVQIHGVGHIGLIMNSQVNSLIKEGLNGGQNTN	180

RESULT 15

AAU83889 standard; protein: 180 AA.

AAU83889;

08-MAY-2002 (first entry)

Bacillus lipase polypeptide #49.

XX Lipase; *Bacillus*; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory; gastrointestinal. XX Synthetic.

XX WO200206457-A2.

XX 24-JAN-2002.

XX 13-JUL-2001; 2001WO-US022160.

XX 13-JUL-2000; 2000US-0217954P.

PR 21-JUN-2001; 2001US-0300378P.

XX (MAXY-) MAXYGEN INC.

XX Giver LJ, Minshull J, Vogel K;

XX PR 13-JUL-2000; 2000US-0217954P.

PR 21-JUN-2001; 2001US-0300378P.

XX (MAXY-) MAXYGEN INC.

XX Giver LJ, Minshull J, Vogel K;

XX DR WPI; 2002-171805/22.

XX DR N-PSDB; ABK33867.

DR

Nucleic acids encoding lipase enzymes which are useful as supplements in animal feeds, as agents of flavor modification and for treating Crohn's disease and celiac disease.

PS

PS Claim 5; Page 145; 196pp; English.

PT The invention relates to new *Bacillus* lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in

PT animal feeds, as agents of flavor modification and fat modification in

PT human foodstuffs (e.g. cheese), as agents in the creation of food

PT emulsifiers, as agents for tanning/processing of leather and as cleaning

PT agents. They are also useful for treating Crohn's disease, cystic

PT fibrosis, coeliac disease, indigestion, obesity and other

PT gastrointestinal mal-absorption problems. Gastrointestinal lipid related

PT conditions can be therapeutically or prophylactically treated via a

PT method of hydrolysing a lipid comprising expressing in a target cell or

PT contacting a target cell with an effective amount of DNA or protein of

PT the invention. Sequences AAU83841-AAU83897 represent *Bacillus* lipase

PT polypeptides of the invention.

XX SQ Sequence 180 AA;

Query Match 97.7%; Score 914; DB 5; Length 180;
Best Local Similarity 96.7%; Pred. No. 2.2e-84;
Matches 174; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

XX Matches 173; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy	1	EEHNPVVMVHIGGASFNFGAKTSVLYSGRSRGKLYAIDFWDKTGTTGNYNNGPVLSRFYKK	60	Qy	1	EEHNPVVMVHIGGASFNFGAKTSVLYSGRSRGKLYAIDFWDKTGTTGNYNNGPVLSRFYKK	60
Db	1	EEHNPVVMVHIGGASFNFGAKTSVLYSGRSRGKLYAIDFWDKTGTTGNYNNGPVLSRFYKK	60	Db	1	EEHNPVVMVHIGGASFNFGAKTSVLYSGRSRGKLYAIDFWDKTGTTGNYNNGPVLSRFYKK	60
Qy	61	VLDETGAKKDIVAHSMGGANTLYKKNLDGGNKVENVVTLGGTNRSTSISKALPGTDNQ	120	Qy	61	VLDETGAKKDIVAHSMGGANTLYKKNLDGGNKVENVVTLGGTNRSTSISKALPGTDNQ	120
Db	61	VLDETGAKKDIVAHSMGGANTLYKKNLDGGNKVENVVTLGGTNRSTSISKALPGTDNQ	120	Db	61	VLDETGAKKDIVAHSMGGANTLYKKNLDGGNKVENVVTLGGTNRSTSISKALPGTDNQ	120
Qy	121	KILYTSIYSSADMIVNNYLSSLDGAKNVQIHGVGHIGLIMNSQVNSLIKEGLNGGQNTN	180	Qy	121	KILYTSIYSSADMIVNNYLSSLDGAKNVQIHGVGHIGLIMNSQVNSLIKEGLNGGQNTN	180
Db	121	KILYTSIYSSADMIVNNYLSSLDGAKNVQIHGVGHIGLIMNSQVNSLIKEGLNGGQNTN	180	Db	121	KILYTSIYSSADMIVNNYLSSLDGAKNVQIHGVGHIGLIMNSQVNSLIKEGLNGGQNTN	180

RESULT 16

AAU83889 standard; protein: 180 AA.

AAU83889;

08-MAY-2002 (first entry)

Bacillus lipase polypeptide #49.

XX Lipase; *Bacillus*; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory; gastrointestinal. XX Synthetic.

XX WO200206457-A2.

XX 24-JAN-2002.

XX 13-JUL-2001; 2001WO-US022160.

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XX (MAXY-) MAXYGEN INC.

XX Giver LJ, Minshull J, Vogel K;

XX DR WPI; 2002-171805/22.

DR N-PSDB; ABK33867.

DR

XX Nucleic acids encoding lipase enzymes which are useful as supplements in
 PT animal feeds, as agents of flavor modification and for treating Crohn's
 PT disease and celiac disease.
 XX

PS Claim 5; Page 145; 196pp; English.

XX The invention relates to new *Bacillus* lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU3841-AAU83897 represent *Bacillus* lipase polypeptides of the invention.

XX Sequence 180 AA:

Qy	Db	Score	Match	Length
		97.2%	910; DB 5;	180;
		Best Local Similarity	97.2%;	Pred. No. 2.8e-84;
		Matches	175;	Conservative 1;
		Mismatches	4;	Indels 0;
		Gaps	0;	
Qy	1	EEHNPVVMHGGGASENFAIGKSTVLSQEWRSRGKLYAIDFWDTGTYNNGRPLSREVKK	60	
Db	1	EEHNPVVMHGGGAAFNPAIGKSTVLSQWRSRGKLYAIDFWDTGTYNNGRPLSREVKK	60	
Qy	61	VLDEETGAKVTDIVAHSMGGANTLYTKNLDGGKNTVQHGKVNVTLLGCTNRSITSKALPQTDPNQ	120	
Db	61	VLDEETGAKVTDIVAHSMGGANTLYTKNLDGGKNTVQHGKVNVTLLGCTNRSITSKALPQTDPNQ	120	
Qy	121	KILYTSIYSSADMIVNYSKLDGAKNVQHGKVNVTLLGCTNRSITSKALPQTDPNQ	180	
Db	121	KILYTSIYSSADMIVNYSKLDGAKNVQHGKVNVTLLGCTNRSITSKALPQTDPNQ	180	

Search completed: April 23, 2004, 10:11:56
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